

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:02 ; Search time 26.1438 Seconds
(without alignments)
614.609 Million cell updates/sec

Title: US-10-049-182-4
Perfect score: 870
Sequence: 1 MHWGTLGFLWLPYLVYQ.....SRLOSLQDMLWQLDLSPGC 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	167	1 LTHU	leptin precursor -
2	854.5	98.2	166	2 I53166	leptin precursor -
3	704	80.9	167	1 L7MS	leptin precursor -
4	690	79.3	167	1 LPTT	leptin precursor -
5	690	78.3	167	2 I55622	rat ob - rat
6	84	9.7	639	2 AI0055	probable soluble 1
7	81.5	9.4	226	2 AC1868	hypothetical prote
8	81.5	9.4	1600	2 AC3281	glutamate dehydrog
9	81	9.3	462	2 JC5625	14-nm filament pro
10	80.5	9.3	444	2 S54039	hypothetical prote
11	79.5	9.1	296	2 D85111	ATP-dependent RNA
12	79.5	9.1	696	2 S4912	hypothetical prote
13	79	9.1	409	2 B89954	hypothetical prote
14	79	9.1	829	2 T01362	probable myosin he
15	79	9.1	952	2 H84583	hypothetical prote
16	79	9.1	1364	2 T40839	hypothetical prote
17	78	9.0	420	2 S75514	sensory transducti
18	78	9.0	421	2 AB2959	exopolysaccharide
19	78	9.0	423	2 D98324	exopolysaccharide
20	78	9.0	2513	2 G96536	hypothetical prote
21	77.5	8.9	460	2 F90097	hypothetical prote
22	77.5	8.9	574	1 B42374	phosphotransferase
23	77.5	8.9	1036	2 D70117	acriflavine resist
24	77	8.9	628	2 A82889	hypothetical prote
25	76.5	8.8	173	2 S77486	ribosomal protein
26	76.5	8.8	362	2 A83967	carbamoyl-phosphat
27	76.5	8.8	600	2 AE0233	lipoprotein inner
28	76.5	8.8	600	2 T47045	hypothetical prote
29	76.5	8.8	600	2 T17437	ybtP protein - Yer

30	76.5	8.8	674	2 S46092	probable membrane
31	76.5	8.8	822	2 E86305	probable trehalose
32	76	8.7	142	2 C72430	hypothetical prote
33	76	8.7	327	2 AH2312	glycine cleavage r
34	76	8.7	570	2 T46011	hypothetical prote
35	76	8.7	995	2 H59432	RhOGAP protein hom
36	75.5	8.7	403	2 T36551	hypothetical prote
37	75.5	8.7	845	2 H13117	probable methyl-ac
38	75.5	8.7	1438	2 S59792	probable membrane
39	75	8.6	296	2 D70424	5,10-methylenetet
40	75	8.6	424	2 E81358	glutamate-1-semial
41	75	8.6	790	2 H71509	phenylalanine-tRNA
42	75	8.6	1191	2 S76414	beta transducin-li
43	74.5	8.6	534	2 B69896	methyl-accepting c
44	74.5	8.6	559	2 AB2202	hypothetical prote
45	74	8.5	177	2 A28106	prolactin, 20K - M

ALIGNMENTS

RESULT 1

LTHU
leptin precursor - human
N/Alternate names: obese protein; obesity factor
C/Species: Homo sapiens (man)
C/Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C/Accession: A38952; J00148
R/Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A/Title: Positional cloning of the mouse obese gene and its human homologue.
A/Reference number: S50863; MUID:95075453; PMID:7984236
A/Accession: A38952
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-167 <ZHA>
A/Cross-references: UNIPROT:P41159; GI:U18915; NID:G623331; PIDN:AAA60470.1; PID:G62333.
R/Liao, H.J.; Deng, Y.B.; Chen, X.M.; Ye, Y.Z.
Chinese Biochem. J. 13, 249-253, 1997
A/Title: Cloning of Chinese obesity gene and construction of prokaryotic expression vec
A/Reference number: J00148
A/Accession: J00148
A/Molecule type: mRNA
A/Residues: 'M', 22-167 <LIA>
A/Experimental source: adipose
A/Note: the author translated GAC for residue 148 as Ser
C/Genetics:
A/Gene: GDB:LEP; OB; OBS
A/Cross-references: GDB:136420; OMIM:164160
A/Map position: 7q31.3-7q31.3
C/Superfamily: leptin
C/Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 100.0%; Score 870; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.8e-70;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MHWGTLGFLWLPYLVYQAVPIQKVODDTKTLKTVTRINDISHTQSVSSKQKVTGL	60
DB	1	MHWGTLGFLWLPYLVYQAVPIQKVODDTKTLKTVTRINDISHTQSVSSKQKVTGL	60
QY	61	DFIPGLHPILTLTKNDQTLAVYQQILTSMPNSRVQISNDLENLRLDLLHLVAFSKSCHLP	120
DB	61	DFIPGLHPILTLTKNDQTLAVYQQILTSMPNSRVQISNDLENLRLDLLHLVAFSKSCHLP	120
QY	121	WASGLETLDSLGVLVLEASGYSTEVALSRLOSLQDMLWQLDLSPGC	167
DB	121	WASGLETLDSLGVLVLEASGYSTEVALSRLOSLQDMLWQLDLSPGC	167

RESULT 2

```
I53166
leptin precursor - human
N:Alternate names: obese
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: I53166; G02328
R:Masuzaki, H.; Ogawa, Y.; Isse, N.; Satoh, N.; Okazaki, T.; Shigemoto, M.; Mori, K.; Tanabe, T.;
Diabetes 44, 855-858, 1995
A:Title: Human obese gene expression. Adipocyte-specific expression and regional difference
A:Reference number: I53166; MUID:95309556; PMID:7789654
A:Accession: I53166
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-166 <RES>
A:Cross-references: UNIPROT:P41159; GB:D49487; NID:G904211; PIDN:BAA08448.1; PID:G904212
R:Chehab, F.F.; Lim, M.E.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01063
A:Accession: G02328
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-166 <CHE>
A:Cross-references: EMBL:U43415; NID:G1163105; PIDN:AAC31660.1; PID:G1163106
C:Genetics:
A:Gene: GDB:LEP; OB; OBS
A:Cross-references: GDB:136420; OMIM:164160
A:Map position: 7q32.1-7q32.1
A:Introns: 48/3
C:Superfamily: leptin

Query Match 98.2%; Score 854.5; DB 2; Length 166;
Best Local Similarity 99.4%; Pred. No. 4.3e-69;
Matches 166; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MHWGTLGFLWLPVLFYVQVPIQKVQDDTKTIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLGFLWLPVLFYVQVPIQKVQDDTKTIKTIVTRINDISHT-SVSSKQKVTGL 59

QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENRLDLHLVLAFSKSLP 120
DB 60 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENRLDLHLVLAFSKSLP 119

QY 121 WASGLETLDSLGVLASGYSTEVVALSRLOGLSQDMLWQLDLSGPC 167
DB 120 WASGLETLDSLGVLASGYSTEVVALSRLOGLSQDMLWQLDLSGPC 166

RESULT 3
LITMS
leptin precursor - mouse
N:Alternate names: obese protein
C:Species: Mus musculus (house mouse)
C>Date: 14-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: S50863
R:Zhang, Y.; Froenica, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A:Title: Positional cloning of the mouse obese gene and its human homologue.
A:Reference number: S50863; MUID:95075453; PMID:7984236
A:Accession: S50863
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-167 <ZHA>
A:Cross-references: UNIPROT:P41160; EMBL:U18812; NID:G746416; PIDN:AAA64564.1; PID:G6032
C:Superfamily: leptin
C:Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 80.9%; Score 704; DB 1; Length 167;
Best Local Similarity 83.2%; Pred. No. 1.2e-55;
Matches 139; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MHWGTLGFLWLPVLFYVQVPIQKVQDDTKTIKTIVTRINDISHTQSVSSKQKVTGL 60
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Db 1 MCVRLCFLWLSYLVQVPIQKVQDDTKTIKTIVTRINDISHTQSVAKQRTGL 60
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENRLDLHLVLAFSKSLP 120
DB 61 DFIPGLHPILTSLKMDQTLAVYQQVLTSLPSONVLIANDLENRLDLHLVLAFSKSLP 120
QY 121 WASGLETLDSLGVLASGYSTEVVALSRLOGLSQDMLWQLDLSGPC 167
DB 120 QTRGLQKPESLDGVLASLYSTEVVALSRLOGLSQDILQQLDLSPEC 167

RESULT 4
LITRT
leptin precursor - rat
N:Alternate names: obese protein; obesity factor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: PC4034; JC4142
R:Funahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Noza-
Biochem. Biophys. Res. Commun. 211, 469-475, 1995
A:Title: Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial h
A:Reference number: PC4034; MUID:95314614; PMID:7794258
A:Accession: PC4034
A:Molecule type: mRNA
A:Residues: 1-167 <FUN>
A:Cross-references: UNIPROT:P50596
A:Experimental source: adipose tissue
A:Note: The authors translated the codon AAA for residue 32 as Thr
R:Murakami, T.; Shima, K.
Biochem. Biophys. Res. Commun. 209, 944-952, 1995
A:Title: Cloning of rat obese cDNA and its expression in obese rats.
A:Reference number: JC4142; MUID:95251725; PMID:7733988
A:Accession: JC4142
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-167 <MUR>
A:Cross-references: DDBJ:D49653; NID:G995614; PIDN:BAA08529.1; PID:G995615
A:Experimental source: liver
C:Comment: This protein is proposed to function as part of a signalling pathway from adi
C:Genetics:
A:Gene: Obese
C:Superfamily: leptin
C:Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 79.3%; Score 690; DB 1; Length 167;
Best Local Similarity 82.0%; Pred. No. 2.1e-54;
Matches 137; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 MHWGTLGFLWLPVLFYVQVPIQKVQDDTKTIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MCVRLCFLWLSYLVQVPIQKVQDDTKTIKTIVTRINDISHTQSVARQRTGL 60
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENRLDLHLVLAFSKSLP 120
DB 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSONVLIANDLENRLDLHLVLAFSKSLP 120
QY 121 WASGLETLDSLGVLASGYSTEVVALSRLOGLSQDMLWQLDLSGPC 167
DB 120 QTRGLQKPESLDGVLASLYSTEVVALSRLOGLSQDILQQLDLSPEC 167

RESULT 5
I55622
rat ob - rat
C:Species: Rattus sp. (rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I55622
R:Ogawa, Y.; Masuzaki, H.; Isse, N.; Okazaki, T.; Mori, K.; Shigemoto, M.; Satoh, N.; Tan-
J. Clin. Invest. 96, 1647-1652, 1995
A:Title: Molecular cloning of rat obese cDNA and augmented gene expression in genetically,
```



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RESULT 12
S44912
hypothetical protein ZK686.2 - Caenorhabditis elegans
N:Contains: hypothetical protein Z97.2
C:Species: Caenorhabditis elegans
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S44912; S44884
R;Du, Z.
submitted to the EMBL Data Library, June 1993
A:Description: Sequence of the C. elegans cosmid ZK686.
A:Reference number: S44909
A:Accession: S44912
A:Molecule type: DNA
A:Residues: 1-696 <DUZ>
A:Cross-references: UNIPROT:P34668; EMBL:L117337; NID:G304345; PIDN:AAA28223.1; PID:G3043
A:Experimental source: cosmid ZK686
R;Du, Z.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZC97.
A:Reference number: S44615
A:Accession: S44884
A:Molecule type: DNA
A:Residues: 401-696 <DUW>
A:Cross-references: EMBL:L114714; NID:Q289737; PIDN:AAA28179.1; PID:Q289738
A:Experimental source: cosmid ZC97
A:Note: designated as ZC97.2 protein
C:Genetics:
A:Introns: 15/1; 89/3; 102/3; 120/3; 145/3; 194/2; 312/2; 453/3; 643/2
C:Keywords: ANP; nucleotide binding; P-loop
F:266-273/Region: nucleotide-binding motif A (P-loop)
F:373-378/Region: nucleotide-binding motif B
F:377-380/Region: DEAD motif
F:401-696/Product: hypothetical protein ZC97.2 #status predicted <ZCP>

Query Match          9.1%; Score 79.5; DB 2; Length 696;
Best Local Similarity 29.2%; Pred. No. 39;
Matches 33; Conservative 12; Mismatches 31; Indels 37; Gaps 6;

Qy 10 LWLW----PYLYVQVAVPIQKVDQDTKLTIKTIIVTRINDISHT-----QSVSSKOKVT 58
Db 433 LHLWNLKPRIFSATAVS-----VKDITSGIPQVDHVSGRALPSSISHRLVVT 481

Qy 59 GLOFIPGLPILTSKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVL 111
Db 482 D----PKFHP-----LAVYQQITRNKFNRTLIFV-NEVSSNRLAHVL 519

RESULT 13
B89954
hypothetical protein SA1524 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89954
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: B89758; MUID:21311952; PMID:11418146
A:Accession: B89954
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <KUR>
A:Cross-references: UNIPROT:Q99TG1; GB:BA000018; PID:G13701497; PIDN:BAB42791.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
C:Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match          9.1%; Score 79; DB 2; Length 409;
Best Local Similarity 21.3%; Pred. No. 22;
Matches 38; Conservative 36; Mismatches 56; Indels 48; Gaps 8;
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Qy 19 VOAVPIQKVDQDTKLTIKTIIV-----TRINDISHTQSVSSKOKVTGLDFIPGLH--- 67
Db 101 INGVPALNTTDTTEIIKTKVLEPNYGGINLEDISAPRCFEIERLKKTETNPVPHDDQ 160
Qy 68 ---PILTSKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLH-----VLAFSKSCHL 119
Db 161 HGTAIVTMAGLVNALRV-----VNKDIKIKVVLNGAGAAGIAIVK---L 202
Qy 120 PWASGLETL---DSLGGVLEASGY---STEVVA-----LSRLQGSLOQMLQMLDSPG 166
Db 203 LYAYGVNVMWCDRSGAIFEGRSYGMNPTKDVAKWTKNKDKIEGSLSEVVKDADVFVG 260

RESULT 14
T01362
probable myosin heavy chain At2g34730 - Arabidopsis thaliana
N:Alternate names: hypothetical protein T29F13.6
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01362; C84760
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
A:Reference number: Z14179
A:Accession: T01362
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-829 <ROU>
A:Cross-references: UNIPROT:O64584; EMBL:AC003096; NID:G3132469; PID:G3132472
A:Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617157
A:Accession: C84760
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-829 <STO>
A:Cross-references: GB:AE002093; NID:G3132472; PIDN:AAC16261.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g34730; T29F13.6
A:Map position: 2
A:Introns: 728/2; 770/3

Query Match          9.1%; Score 79; DB 2; Length 829;
Best Local Similarity 21.5%; Pred. No. 54;
Matches 34; Conservative 27; Mismatches 45; Indels 52; Gaps 6;

Qy 24 IQKVQDDTKLTIKTIIVTRINDISHTQSVSSKOKVTGLDFIPGLHFLTSLKMDQTLAVY- 82
Db 57 ISRVVSD--SIIRGWTAIES-----DAAEKIAQKD-----LELSKIRETLTLLYH 99

Qy 83 -----QOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLP 120
Db 100 VGSBENESESRLIHDELITQGSSESSKKKARKKQKMLVLEELTNLREYTHIN----- 150
Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOQSLQDML 158
Db 151 -GSGATVDDSLG--LDSSPHETRSKTVDMKLDLSKSL 185

RESULT 15
H84583
hypothetical protein At2g20010 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84583
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:44:03 ; Search time 124.85 Seconds
(without alignments)
517.333 Million cell updates/sec

Title: US-10-049-182-4
Perfect score: 870
Sequence: 1 MHWTGTCFLWLPYFYVQ.....SRQGSQDMLWQLDLSPGC 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	870	100.0	167	AAW03694	Human obe
2	870	100.0	167	AAW03694	Human obe
3	870	100.0	167	AAW03694	Human obe
4	870	100.0	167	AAW03694	Human obe
5	870	100.0	167	AAW03694	Human obe
6	870	100.0	167	AAW03694	Human obe
7	870	100.0	167	AAW03694	Human obe
8	870	100.0	167	AAW03694	Human obe
9	870	100.0	167	AAW03694	Human obe
10	870	100.0	167	AAW03694	Human obe
11	870	100.0	167	AAW03694	Human obe
12	870	100.0	167	AAW03694	Human obe
13	870	100.0	167	AAW03694	Human obe
14	870	100.0	167	AAW03694	Human obe
15	870	100.0	167	AAW03694	Human obe
16	870	100.0	167	AAW03694	Human obe
17	870	100.0	167	AAW03694	Human obe
18	870	100.0	167	AAW03694	Human obe
19	870	100.0	167	AAW03694	Human obe
20	870	100.0	167	AAW03694	Human obe
21	870	100.0	167	AAW03694	Human obe
22	870	100.0	167	AAW03694	Human obe
23	870	100.0	167	AAW03694	Human obe
24	870	100.0	167	AAW03694	Human obe
25	870	100.0	167	AAW03694	Human obe

26	870	100.0	167	ADH21373	Human lep
27	870	100.0	167	ADH21372	Human lep
28	870	100.0	167	ADH21371	Human lep
29	870	100.0	167	ADH17068	Human lep
30	870	100.0	167	ADK119923	Human lep
31	870	100.0	167	ADQ24730	Human lep
32	870	100.0	167	ADQ19663	Human sof
33	870	100.0	396	AAW10534	Leptin 1-
34	870	100.0	396	AAW10535	Leptin 1-
35	870	100.0	397	AAW22722	Human obe
36	870	100.0	397	AAW24060	Human obe
37	870	100.0	397	ADQ29344	Human obe
38	870	100.0	397	ADC08948	Human obe
39	870	100.0	397	ADC78787	Human PRO
40	870	100.0	399	AAW10536	Leptin 1-
41	870	100.0	401	AAW10537	Leptin 1-
42	870	100.0	752	ADP15039	Human alb
43	870	100.0	752	ADH21302	Human alb
44	866	99.5	167	AAU02994	Human Ob
45	866	99.5	167	AAU02989	Human Ob

ALIGNMENTS

RESULT 1
AAW03694
ID AAW03694 standard; protein; 167 AA.
XX
AC AAW03694;
XX
DT 15-JUL-1997 (first entry)
XX
DE Human obese (ob) protein.
XX
KW Human; obese; ob; body; weight; modulation; defect; mutation; prevention;
interference; production; function; treatment; control; obesity; disease;
reduction; food intake; gain; mammal; type II; diabetes; mellitus;
hypertension; hyperlipidaemia; hyperlipidemia; identification; receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Peptide /label= sig_peptide
FT Peptide 22..167
FT Peptide /label= mat_peptide
XX
EP741187-A2.
XX
PD 06-NOV-1996.
XX
PF 24-APR-1996; 96EP-00106408.
XX
PR 05-MAY-1995; 95US-00435777.
PR 07-JUN-1995; 95US-00484629.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Campfield A, Devos R, Guisez Y;
XX
WPI; 1996-487390/49.
XX
DR N-PSDB; AAT42168.
XX
PT New isolated human and murine obese proteins - and related DNA, used for
the treatment, prevention and control of obesity and associated diseases.
XX
PS Claim 3; Page 28-29; 36pp; English.
XX
CC The present sequence is the human obese (ob) protein, a body weight
modulator, which can be administered to patients suffering from ob gene
defects or mutations which prevent or interfere with its production
and/or function. The ob protein can be used to treat, prevent or control

CC obesity and associated diseases by reducing food intake and weight gain
CC in mammals. It can also be used to treat related conditions such as type
CC II diabetes mellitus, hypertension and hyperlipidaemia, and to identify
CC ob protein receptors. The human ob gene was isolated by screening a
CC lambda phage cDNA library, made from human adipocyte tissue derived RNA,
CC with a murine ob gene obtained using the methods of Zhang, Y. et al.,
CC Nature 372, 425-432 (1994)
XX
SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
Db 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
Qy 121 WASGLETLDSLGVLGASGYSTEVVALSRQGSLODMLWQDLSPGC 167
Db 121 WASGLETLDSLGVLGASGYSTEVVALSRQGSLODMLWQDLSPGC 167

RESULT 2

AAR99473
ID AAR99473 standard; protein; 167 AA.

XX AC AAR99473;
XX DT 22-OCT-1996 (first entry)
XX DE Human ob protein.
XX KW Obesity; ob gene; ob protein; appetite suppression factor.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Protein /label= Sig_peptide
XX FT Protein /label= Mat_protein

XX WO9622308-A2.

XX 25-JUL-1996.

XX 22-JAN-1996; 96WO-US001471.

XX 20-JAN-1995; 95US-00377068.

XX 10-APR-1995; 95US-00419214.

XX 07-JUN-1995; 95US-00486450.

XX 07-JUN-1995; 95US-00486459.

XX 07-JUN-1995; 95US-00487111.

XX 04-OCT-1995; 95US-00540242.

XX (ZYMO) ZYMOGENETICS INC.

XX (UNIW) UNIV WASHINGTON.

XX Weigle DS, Kuiper JL, Bukowski TR;

XX WPI; 1996-354476/35.

XX N-PSDB; AAT34164.

XX Identifying factors that regulate appetite, e.g. for treatment of obesity

XX - by administering a test sample to a mammal and determining decrease in

XX food consumption.

XX The human ob protein (appetite suppression factor) amino acid sequence
CC (AAR99473) was deduced from a cDNA clone (AAT34164) derived from human
CC adipose tissue. The mature ob protein, pref. modified with an N-terminal
CC histidine tag, can be obtd. by expression in transformed host (esp.
CC yeast) cells. It is used to regulate the appetite of an individual,
CC thereby decreasing food consumption. Mouse ob proteins (see also AAR99472
CC and AAR99474) were also identified

XX SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
Db 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
Qy 121 WASGLETLDSLGVLGASGYSTEVVALSRQGSLODMLWQDLSPGC 167
Db 121 WASGLETLDSLGVLGASGYSTEVVALSRQGSLODMLWQDLSPGC 167

RESULT 3

AAR92720
ID AAR92720 standard; protein; 167 AA.

XX AC AAR92720;

XX DT 12-SEP-1996 (first entry)

XX DE Obesity protein.

XX KW Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
XX food intake; energy expenditure; high blood pressure; cholesterol; human;
XX Gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Protein /note= "signal peptide"
XX FT Protein /note= "obesity protein"

XX GB2292382-A.

XX 21-FEB-1996.

XX 17-AUG-1995; 95GB-00016947.

XX 17-AUG-1994; 94US-00292345.

XX 30-NOV-1994; 94US-00347563.

XX 10-MAY-1995; 95US-00438431.

XX 07-JUN-1995; 95US-00483211.

XX (UYRQ) UNIV ROCKEFELLER.

XX Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;

XX Burley SK;

XX WPI; 1996-099009/11.

XX N-PSDB; AAT16373.

XX Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
XX reducing wt. in treatment of diabetes, high blood pressure and high
XX cholesterol and for cosmetic reasons.

PS Claim 2; p171-172; 304pp; English.

CC This sequence represents the human obesity polypeptide (OBP). OBP (also known as leptin) is a hormone involved in the regulation of body weight.

CC This sequence has effects on both food intake and energy expenditure. OBP and its analogues are useful for modifying body weight (optionally combined with known medicaments), for treating diabetes, high blood pressure or high cholesterol. The DNA encoding this sequence (and sequences complementary to it) can be used in gene therapy for modifying body weight. This protein can be used for reducing weight for health or cosmetic reasons in obese humans, or to produce leaner food animals.

CC Antagonists of OBP (including antibodies) are useful for increasing body weight, e.g. for treating weight loss associated with cancer, or for cosmetic reasons in humans, or for production of Kobe beef or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP complexes enables in vitro evaluation of levels of OBP in a sample, especially to detect diseases associated with elevated or decreased levels, and to monitor treatment of these diseases

XX Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTCGLFWLWPLYFYQVAPVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTCGLFWLWPLYFYQVAPVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

Qy 61 DFIFGLHPILTLTKMDQTLAVYQOILTSMPERNVIOISNDLENRLDLHLVLAFSKSCHLP 120
Db 61 DFIFGLHPILTLTKMDQTLAVYQOILTSMPERNVIOISNDLENRLDLHLVLAFSKSCHLP 120

Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRQSLQSLQDMLWQLDLSPGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVALSRQSLQSLQDMLWQLDLSPGC 167

RESULT 4
AAW34060
ID AAW34060 standard; protein; 167 AA.
AC AAW34060;
XX 24-APR-1998 (first entry)
XX Human obese (ob) protein.
XX Obese protein; ob protein; osteogenic cell; bone-forming activity; migration; bone-forming cell; marrow mesenchymal cell; bone repair; bone healing; bone loss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..21
XX /note= "signal peptide"
XX WO9739767-A1.
XX 30-OCT-1997.
XX 18-APR-1997; 97WO-US006892.
XX 19-APR-1996; 96US-0015647P.
XX (ZYMO) ZYMOGENETICS INC.
XX (UNIW) UNIV WASHINGTON.
XX Durnam DM, Kuijper JL, Weigle DS, Liu CC;
XX WPI; 1997-535577/49.

DR N-PSDB; AAT93021.

XX Use of obese protein for inducing bone formation - particularly for treating osteoporosis, repairing fractures, dental defects or resectioning due to oncogenesis.

PS Disclosure; Page 32; 42pp; English.

XX The present sequence represents a human obese (ob) protein. DNA sequence was isolated from an adipose tissue cDNA library using a probe derived from the mouse obese gene. ob proteins can produce a dramatic increase in osteogenic cells or their bone-forming activity. They can enhance recruitment or migration of bone-forming cells to the proper bone-forming tissues and tissue sites. The ob protein was used in the method of the invention, which involves the stimulation of a cell population containing marrow mesenchymal cells. The method comprises exposing the cell population to an ob protein for expansion of osteogenic cells, a biological fluid obtained from an ob protein-treated mammal, or a culture medium that has been conditioned by growth of endocrine or CNS cells or tissue exposed to ob protein. The method can be used in a mammal for promoting bone repair or bone healing, stimulating bone ingrowth into a prosthetic device or dental implant that has been inserted into a mammal, for treating bone loss, for increasing bone length, for stimulating active bone growth, or for inducing bone formation

XX Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTCGLFWLWPLYFYQVAPVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTCGLFWLWPLYFYQVAPVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

Qy 61 DFIFGLHPILTLTKMDQTLAVYQOILTSMPERNVIOISNDLENRLDLHLVLAFSKSCHLP 120
Db 61 DFIFGLHPILTLTKMDQTLAVYQOILTSMPERNVIOISNDLENRLDLHLVLAFSKSCHLP 120

Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRQSLQSLQDMLWQLDLSPGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVALSRQSLQSLQDMLWQLDLSPGC 167

RESULT 5
AAW57442
ID AAW57442 standard; peptide; 167 AA.
AC AAW57442;
XX 10-AUG-1998 (first entry)
XX Human leptin sequence.
XX Leptin; murine; antagonist; treatment; type II diabetes; insulin; human.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Disulfide-bond 7..167
XX /note= "disulphide bridge"
XX WO9812224-A1.
XX 26-MAR-1998.
XX 15-SEP-1997; 97WO-EP005035.
XX 20-SEP-1996; 96DE-01038487.
XX (FARH) HOECHST AG.
XX Ertl J, Freibisch G, Mueller G;

XX WPI; 1998-217209/19.
 XX Use of leptin antagonists - for restoring or amplifying the physiological
 PT effect of insulin in the treatment of Type II diabetes.
 XX Disclosure; Page 19; 30pp; English.

XX This is a human leptin protein sequence which is highly homologous to the
 CC murine leptin sequence. The carboxyl-terminal fragment of the murine
 CC leptin can act as a leptin antagonist. This can be used in a
 CC pharmaceutical composition which comprises the murine leptin fragment
 CC which is therapeutically beneficial for the treatment of Type II
 CC diabetes. The leptin antagonists include peptides derived from leptin
 CC fragments and may be obtained by chemically or enzymatically cleaving
 CC intact leptin or by recombinant expression using microorganisms. This
 CC fragment can be prepared by digestion of leptin with lysyl endopeptidase.
 CC The leptin antagonists can restore or amplify the physiological effect of
 CC insulin by inhibiting leptin-induced insulin resistance

XX Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWTLCGFLWLPYLFYVQAVPIQKVQDDTKLIKIVTRINDISHTQSVSSKQKVTGL 60
 Db 1 MHWTLCGFLWLPYLFYVQAVPIQKVQDDTKLIKIVTRINDISHTQSVSSKQKVTGL 60
 Qy 61 DFIPGLHPILTSLKMDQTLAVYQIILTSMPSRNVIQISNDLENRLDLLHLVAFSKSCHLP 120
 Db 61 DFIPGLHPILTSLKMDQTLAVYQIILTSMPSRNVIQISNDLENRLDLLHLVAFSKSCHLP 120
 Qy 121 WASGLETLDSLGVLASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167
 Db 121 WASGLETLDSLGVLASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167

RESULT 6

AY82110
 ID AAY82110 standard; protein; 167 AA.

AC AAY82110;

DT 05-JUN-2000 (first entry)

DE Human obese protein SEQ ID NO:5.

XX Ob gene; ob protein; obesity; body weight; polyethylene; obese protein;
 KW polypropylene; protein conjugate; anorectic.

XX Homo sapiens.

XX US6025324-A.

XX 15-FEB-2000.

XX 15-MAY-1996; 96US-00648262.

XX 15-MAY-1996; 96US-00648262.

XX (HOFF) HOFFMANN LA ROCHE INC.

XX Bailon PS, Devos R, Campfield A, Guisez Y;

XX WPI; 2000-222636/19.

DR N-PSDB; AAZ95530.

XX Polyethylene and polypropylene obese protein conjugates are useful for
 PT the prevention, treatment and control of obesity and associated diseases
 PT and conditions.

XX

PS Disclosure; Col 35-36; 26pp; English.

XX The present invention describes a composition comprising one or more
 CC polyethylene and polypropylene human obese protein conjugates (I). The
 CC composition has anorectic activity. The conjugates are used for the
 CC treatment, prevention and control of obesity and associated conditions in
 CC humans and animals. The present sequence represents the human obese
 CC protein

XX Sequence 167 AA;

Query Match 100.0%; Score 870; DB 3; Length 167;
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWTLCGFLWLPYLFYVQAVPIQKVQDDTKLIKIVTRINDISHTQSVSSKQKVTGL 60

Db 1 MHWTLCGFLWLPYLFYVQAVPIQKVQDDTKLIKIVTRINDISHTQSVSSKQKVTGL 60

Qy 61 DFIPGLHPILTSLKMDQTLAVYQIILTSMPSRNVIQISNDLENRLDLLHLVAFSKSCHLP 120

Db 61 DFIPGLHPILTSLKMDQTLAVYQIILTSMPSRNVIQISNDLENRLDLLHLVAFSKSCHLP 120

Qy 121 WASGLETLDSLGVLASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167

Db 121 WASGLETLDSLGVLASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167

RESULT 7

AAB28448

ID AAB28448 standard; protein; 167 AA.

XX AAB28448;

XX 01-FEB-2001 (first entry)

XX Human OB polypeptide.

XX Human; mouse; OB gene; obesity; adiposity; body weight.

XX Homo sapiens.

XX US6124448-A.

XX 26-SEP-2000.

XX 07-JUN-1995; 95US-00488208.

XX 17-AUG-1994; 94US-00292345.

XX 30-NOV-1994; 94US-00347563.

XX 10-MAY-1995; 95US-00438431.

XX (UYRQ) UNIV ROCKEFELLER.

XX Maffei M, Proenca R, Zhang Y, Friedman JM;

XX WPI; 2000-601556/57.

XX N-PSDB; AAC62566.

XX Nucleic acid primers and probes useful for detecting mutations in

XX mammalian OB gene associated with regulation of body weight and

XX adiposity.

XX Example; Fig 3; 153pp; English.

XX The present sequence is encoded by a nucleotide sequence used in an
 CC invention relating to the control of body weight of animals including
 CC humans. Nucleic acids of at least 10 nucleotides which are hybridisable
 CC to a non-coding region of an OB nucleic acid have been created. The OB
 CC gene plays a critical role in the regulation of body weight and
 CC adiposity. The nucleic acids may be used as probes or as primers for PCR.
 CC They are useful for evaluating the presence of mutations in the human OB
 CC gene or for evaluating the level of expression of OB mRNA. Defects

CC associated with OB gene expression result in obese phenotypes
XX
SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVDKTKLTKITVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVQAVPIQKVDKTKLTKITVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLP 120
Db 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLP 120
Qy 121 WASGLETLDSLGVLGASGYSTEVVALSRLOGLQSLQDMLWQLDLSPGC 167
Db 121 WASGLETLDSLGVLGASGYSTEVVALSRLOGLQSLQDMLWQLDLSPGC 167

RESULT 8
AAV84190
ID AAY84190 standard; protein; 167 AA.
XX
AC AAY84190;
DT 03-JUL-2000 (first entry)
XX
DE Amino acid sequence of the primary structure of human leptin.
XX Human; leptin; blood brain barrier; homeostasis; body mass; anorexia;
KW obesity; hyperglycemia; hyperinsulinemia; hyperphagia;
KW thyroid dysfunction; infertility; type II diabetes mellitus;
KW non-insulin-dependent diabetes mellitus; hematopoiesis dysfunction;
KW tumour suppression; weight loss; diet.
XX
OS Homo sapiens.
XX
PN WO200011173-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019021.
XX
PR 21-AUG-1998; 98US-0097457P.
PR 19-AUG-1999; 99US-00377081.
XX
PA (ALBA-) ALBANY MEDICAL COLLEGE.
XX
PI Grasso P, Lee DW, Leinung MC;
XX
XX WPI; 2000-237652/20.
DR
XX Leptin peptides useful for treating pathophysiology relating to
PT homeostasis of body mass such as obesity, anorexia, and hematopoiesis
PT dysfunction and tumor suppression.
XX
PS Claim 26; Fig 16; 121pp; English.
XX
CC The present sequence represents a human leptin. The specification
CC describes peptides derived from leptin. The leptin-derived peptides have
CC increased ability to cross the blood brain barrier and improved bio-
CC availability. Peptides derived from leptin are useful for treating and
CC preventing pathophysiology relating to homeostasis of body mass such as
CC anorexia, obesity comprising hyperglycemia, hyperinsulinemia,
CC hyperphagia, thyroid dysfunction, infertility, type II diabetes mellitus
CC and non-insulin-dependent diabetes mellitus (NIDDM), and hematopoiesis
CC dysfunction and tumor suppression. The peptides are also useful for
CC identifying drugs useful in weight loss diet regimen
XX
SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVDKTKLTKITVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVQAVPIQKVDKTKLTKITVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLP 120
Db 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLP 120
Qy 121 WASGLETLDSLGVLGASGYSTEVVALSRLOGLQSLQDMLWQLDLSPGC 167
Db 121 WASGLETLDSLGVLGASGYSTEVVALSRLOGLQSLQDMLWQLDLSPGC 167

RESULT 9
AAY80259
ID AAY80259 standard; protein; 167 AA.
XX
AC AAY80259;
XX
DT 25-MAY-2000 (first entry)
XX
DE Human obese OB protein SEQ ID NO:5.
XX
KW Obese; OB protein; polyethylene; polypropylene; weight; obesity;
KW anorectic; gene therapy; type II diabetes mellitus; hypertension;
KW hyperlipidaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /label= signal
FT /label= OB_protein
XX
PN US6025325-A.
XX
PD 15-FEB-2000.
XX
PF 15-MAY-1996; 96US-00648263.
XX
PR 05-MAY-1995; 95US-00435777.
PR 07-JUN-1995; 95US-00484629.
XX
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Guisez Y, Campfield A, Devos R;
XX
XX WPI; 2000-194674/17.
DR N-PSDB; AAZ91516.
XX
XX Polyethylene glycol conjugated proteins useful for modulating the body
PT weight of humans and animals for the prevention, treatment and control of
PT obesity and associated diseases.
XX
PS Disclosure; Col 39-40; 29pp; English.
XX
CC The present invention describes polyethylene glycol conjugated obese (OB)
CC protein compositions (I) useful for modulating the body weight of humans
CC and animals for the prevention, treatment and control of obesity and
CC associated diseases. (I) have anorectic activity and can be used in gene
CC therapy. (I) may be used for the prevention, treatment and control of
CC obesity and associated diseases such as type II diabetes mellitus,
CC hypertension and hyperlipidaemia. The present sequence represents the
CC human OB protein, which can be used in the production of (I)
XX
SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 3; Length 167;


```
QY 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPGRNVQISNDLENLRDLHLVLAFAKSKCHLP 120
DB 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPGRNVQISNDLENLRDLHLVLAFAKSKCHLP 120

QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSLQSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSLQSLQDMLWQLDLSGPC 167

RESULT 12
AAB59914
ID AAB59914 standard; protein; 167 AA.
XX
AC AAB59914;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human leptin fragment SEQ ID NO: 32.
XX
KW Leptin; human; LSR; lipolysis stimulated receptor; obesity; hypertension;
KW anorexia; cachexia; stroke; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200121647-A2.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-2000; 2000WO-IB001470.
XX
PR 22-SEP-1999; 99US-0155506P.
XX
PA (GEST ) GENSET.
XX
PI Yen F, Erickson MR, Fruebis J, Bihain B;
XX
DR WPI; 2001-218642/22.
XX
PT New leptin polypeptide fragment and related polynucleotides, useful for
PT the prevention and treatment of obesity and obesity-related diseases such
PT as hypertension and diabetes.
XX
PS Claim 1; Page 232-233; 247pp; English.
XX
CC The present invention provides the protein and coding sequences of leptin
CC fragments which modulate the activity of lipolysis stimulated factor
CC (LSR). These sequences are useful in the treatment of obesity related
CC diseases, including obesity, anorexia, cachexia, cardiac and coronary
CC insufficiency, stroke, hypertension, atherosclerotic disease,
CC atherosclerosis, non-insulin dependent diabetes, hyperlipidaemia,
CC hyperuricaemia and syndrome X
XX
SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGCGFLWLPYLFVQVAPVQKQVDDTKTLTKTIVTRINDISHTQSVSSKQKV7GL 60
DB 1 MHWGTLGCGFLWLPYLFVQVAPVQKQVDDTKTLTKTIVTRINDISHTQSVSSKQKV7GL 60

QY 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPGRNVQISNDLENLRDLHLVLAFAKSKCHLP 120
DB 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPGRNVQISNDLENLRDLHLVLAFAKSKCHLP 120

QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSLQSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSLQSLQDMLWQLDLSGPC 167

RESULT 13
```

```
AAB72927
ID AAB72927 standard; protein; 167 AA.
XX
AC AAB72927;
XX
DT 16-MAY-2001 (first entry)
XX
DE Human leptin.
XX
KW Bone resorption modulation; leptin; osteoporosis; Paget's disease;
KW osteoclastogenesis.
XX
OS Homo sapiens.
XX
PN AU200048971-A.
XX
PD 08-FEB-2001.
XX
PF 01-AUG-2000; 2000AU-00048971.
XX
PR 03-AUG-1999; 99AU-00001999.
XX
PA (UYME ) UNIV MELBOURNE.
XX
PI Nicholson GC;
XX
DR WPI; 2001-235416/25.
XX
DR N-PSDB; AAF76679.
XX
PT Modulating bone resorption in human or animal for treating osteoporosis
PT or Paget's disease, comprises administering leptin, its derivative,
PT homologue, analog, chemical equivalent, antagonist or agonist.
XX
PS Claim 3; Page 26-27; 40pp; English.
XX
CC The present invention describes a method of modulating bone resorption
CC comprising administering leptin or a derivative under conditions suitable
CC for the modulation of osteoclastogenesis. This is useful in the treatment
CC of osteoporosis and Paget's disease. The present sequence is the human
CC leptin protein sequence
XX
SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGCGFLWLPYLFVQVAPVQKQVDDTKTLTKTIVTRINDISHTQSVSSKQKV7GL 60
DB 1 MHWGTLGCGFLWLPYLFVQVAPVQKQVDDTKTLTKTIVTRINDISHTQSVSSKQKV7GL 60

QY 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPGRNVQISNDLENLRDLHLVLAFAKSKCHLP 120
DB 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPGRNVQISNDLENLRDLHLVLAFAKSKCHLP 120

QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSLQSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSLQSLQDMLWQLDLSGPC 167

RESULT 14
AAB10338
ID AAB10338 standard; protein; 167 AA.
XX
AC AAB10338;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human leptin (LEP).
XX
KW Mucosal cell; cell therapy; gene therapy; hyperglycaemia; wound healing;
KW haemophilia; eye damage; diabetes; obesity; degenerative disorder; ulcer;
KW beta-cell destruction; kidney tubule calcification; liver degeneration;
```

KW diabetic retinopathy; cancer; coronary heart disease; growth disorder;
 KW dyslipidaemia; coagulation disorder; stroke; peripheral vascular disease;
 KW hypertension; wasting syndrome; passive immunisation; immunosuppressive;
 KW Helicobacter pylori; arthritis; cardiovascular disease; ophthalmological;
 KW hypoglycaemic; anorectic; coagulant; cerebroprotective; antimicrobial;
 KW leptin; LEP; vulnary; cytostatic; hypotensive; cardiant; human.
 XX Homo sapiens.
 OS

XX WO200168828-A2.

XX 20-SEP-2001.

XX 12-MAR-2001; 2001WO-1B000722.

XX 13-MAR-2000; 2000US-0188796P.

XX 08-DEC-2000; 2000US-0254464P.

XX (ENGE-) ENGINE INC.

XX Kieffer TJ, Cheung AT;

XX WPI; 2001-582445/65.

XX N-PSDB; AAD17487.

XX Novel isolated or cultured mucosal cell producing nutrient-regulatable
 PT protein expressed by transgene comprising expression control element
 PT linked with nucleic acid encoding protein, is useful for treating
 PT diabetes.
 XX

XX Disclosure; Fig 17; 75pp; English.

XX The present invention relates to an isolated or cultured mucosal cell
 CC that produces a protein regulatable by a nutrient, where expression of
 CC the protein is conferred by a transgene comprising an expression control
 CC element in operable linkage with a nucleic acid encoding the protein. The
 CC invention is used in cell therapy and gene therapy. Isolated or cultured
 CC mucosal cell is useful for treating a hyperglycaemic condition such as
 CC type 1 diabetes (insulin-dependent diabetes), where the subject has a
 CC fasting plasma glucose level of greater than 110 mg/dl. It is also useful
 CC for treating obesity or undesirable body mass. Preferably, in these
 CC conditions the mucosal cell expresses insulin, leptin, glucagon-like
 CC peptide (GLP)-1, GLP-2, cholecystokinin (CCK), a glucagon antagonist, a
 CC growth hormone, a clotting factor or an antibody. The mucosal cells are
 CC implanted into a mucosal tissue or non-mucosal tissue such as liver,
 CC pancreas or muscle. Mice strains that develop or are susceptible to
 CC developing a particular disease (e.g. diabetes, cancer, degenerative
 CC disorders etc.) are also useful for introducing therapeutic proteins in
 CC order to study the effect of therapeutic protein expression in the
 CC disease susceptible mouse. Mucosal cell is also useful for treating
 CC insulin-independent (type 2) diabetes, degeneration of pancreas (beta-
 CC cell destruction), kidney tubule calcification, degeneration of liver,
 CC eye damage (diabetic retinopathy), diabetic foot, ulcerations in mucosa
 CC such as mouth and gums, excess bleeding, wound healing or delayed blood
 CC coagulation and increased risk of coronary heart disease, stroke,
 CC peripheral vascular disease, dyslipidaemia, hypertension and obesity.
 CC Mucosal cell also produces protein such as clotting factors to treat
 CC haemophilia and other coagulation disorders, growth factors to treat
 CC growth disorders or wasting syndrome, and antibodies to provide passive
 CC immunisation or protection of a subject against foreign antigens or
 CC pathogens e.g. Helicobacter pylori or to provide treatment of cancer,
 CC arthritis, or cardiovascular disease. The present sequence is human
 CC leptin (LEP)
 XX

SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;

Best Local Similarity 100.0%; Pred. No. 4.8e-85;

Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWTGCGFLWLPYLFYQVAPVQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

Db 1 MHWTGCGFLWLPYLFYQVAPVQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

QY 61 DPFGHPIILTSKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
 Db 61 DPFGHPIILTSKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
 QY 121 WASGLETUDSLGGVLEASGYSTEVVALSRLOGLSQDMLWQLDLSPGC 167
 Db 121 WASGLETUDSLGGVLEASGYSTEVVALSRLOGLSQDMLWQLDLSPGC 167

RESULT 15

AAU02890

ID AAU02890 standard; protein; 167 AA.

XX AC AAU02890;

XX DT 12-SEP-2001 (first entry)

XX DE Human Ob protein sequence.

XX KW Ob; haematopoietic cytokine; metabolism; metabolism; weight regulation; inflammation;
 KW appetite regulation; mammalian circulatory system; autoimmunity; cancer;
 KW immunological response; abnormal proliferation; regeneration; human;
 KW degeneration; responsive cell type atrophy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "Signal peptide"

FT Protein /note= "Mature human Ob protein"

XX US6225446-B1.

XX PD 01-MAY-2001.

XX PF 05-DEC-1996; 96US-00759628.

XX PR 06-DEC-1995; 95US-0008574P.

XX SCHE) SCHERING CORP.

XX PI Altman SW, Rock FL, Bazan JF, Kastelein RA;

XX WPI; 2001-327467/34.

XX PT Mutational variants of mammalian Ob proteins, useful e.g. for regulating
 PT weight and appetite, also in screening or treatment of conditions
 PT associated with abnormal proliferation.

XX PS Disclosure; Col 3-4; 24pp; English.

XX CC The sequence represents human Ob protein which belongs to the
 CC haematopoietic cytokine subgroup. Cytokines function in regulating
 CC metabolism and weight by mediating differentiation and other signals
 CC within the mammalian circulatory system. Pure or recombinant mutational
 CC variants of mammalian Ob proteins may therefore be used for the
 CC regulation of weight and appetite. These mutants and antibodies against
 CC them are useful in screening and treatment of conditions associated with
 CC abnormal proliferation, such as cancer, and are of use in situations
 CC where cytokine functions have been implicated, e.g. immunological
 CC responses, inflammation, autoimmunity, regeneration, degeneration and
 CC atrophy of responsive cell types
 XX

SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;

Best Local Similarity 100.0%; Pred. No. 4.8e-85;

Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWTGCGFLWLPYLFYQVAPVQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

Db 1 MHWTLCGFLWLPYLFYVQVPIQKQVDDTKLIKTIIVTRINDISHTSQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVQISNDLENLRDILLHVLAFSKSCHLP 120
Db 61 DFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVQISNDLENLRDILLHVLAFSKSCHLP 120
Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGSLQDMLWOLDLSPGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGSLQDMLWOLDLSPGC 167

Search completed: March 12, 2005, 04:59:47
Job time : 127.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:44:37 ; Search time 120.581 Seconds
(without alignments)
709.207 Million cell updates/sec

Title: US-10-049-182-4

Perfect score: 870

Sequence: 1 MHWGTLGFLWLPYFYVQ.....SRLGSLQDMLWQLDLSFGC 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	167	1	P41159 homo sapien
2	866	99.5	167	1	Q6NT58
3	780	89.7	167	1	OB MACMU
4	733	84.3	146	1	OB PANTR
5	728	83.7	146	1	OB GORGO
6	724	83.2	167	1	OB_FELCA
7	721	82.9	146	1	OB_PONPY
8	715	82.2	167	1	OB_PIG
9	705	81.0	167	1	OB BOVIN
10	704	80.9	167	1	OB_MOUSE
11	690	79.3	167	1	OB_RAT
12	675	77.6	167	1	OB_CANFA
13	640	73.6	163	1	OB_CHICK
14	628	72.2	146	1	OB_T8R8
15	624	71.7	146	1	OB SHEEP
16	588.5	67.6	145	2	Q6S9B2
17	576.5	66.3	145	1	OB_MEIGA
18	551	63.3	167	1	OB_SMICR
19	535	61.5	167	2	Q706D0
20	535	61.5	167	2	Q706D1
21	498	57.2	119	2	Q861R2
22	481	55.3	123	2	Q95KW9
23	477	54.8	118	2	Q8MK60
24	476	54.7	118	2	Q8MKS8
25	474	54.5	118	2	Q8MK59
26	469	53.9	118	2	Q8MK61
27	449	51.6	109	2	Q866S7
28	447	51.4	99	1	OB HORSE
29	439	50.5	109	2	Q864V1
30	387	44.5	106	2	Q95MG5
31	380	43.7	90	2	Q8WMK7

32 376 43.2 90 2 Q7TMN2
33 375 43.1 90 2 Q7TMN0
34 371 42.6 91 2 Q7YR78
35 368 42.3 90 2 Q8WML2
36 367 42.3 90 2 Q8WML1
37 367 42.2 90 2 Q7YQJ8
38 361 41.5 89 2 Q8WML0
39 361 41.5 89 2 Q6YIR1
40 353 40.6 89 2 Q8WMK9
41 343.5 39.5 100 2 Q8UWJ3
42 342 39.3 90 2 Q8WMK8
43 340 39.1 86 2 Q8MJ10
44 330 37.9 90 2 Q7TMN1
45 204 23.4 48 2 Q95MZ8

ALIGNMENTS

RESULT 1

ID OB_HUMAN OB_HUMAN STANDARD; PRT; 167 AA.
AC P41159; O15158;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, last sequence update)
DT 25-OCT-2004 (Rel. 45, last annotation update)
DE Leptin precursor (Obesity factor) (Obese protein).
GN Name=LEP; Synonyms=OB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;
RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RT "Positional cloning of the mouse obese gene and its human homologue."
RL Nature 372:425-432(1994).
RN [2]
RP ERRATUM.
RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RL Nature 374:479-479(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95309556; PubMed=7789654;
RA Masuzaki H., Ogawa Y., Issse N., Satoh N., Okazaki T., Shigemoto M.,
Mori K., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,
Nakao K.;
RT "Human obese gene expression. Adipocyte-specific expression and regional differences in the adipose tissue."
RL Diabetes 44:855-858(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96223958; PubMed=8626726; DOI=10.1074/jbc.271.8.3971;
RA Gong D.W., Bi S., Pratley R.E., Weintraub B.D.;
RT "Genomic structure and promoter analysis of the human obese gene."
RL J. Biol. Chem. 271:3971-3974(1996).
RN [5]
RP SEQUENCE FROM N.A.
RA Chehab F.F., Lim M.E.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=96070903; PubMed=7499240; DOI=10.1074/jbc.270.46.27728;
RA Issse N., Ogawa Y., Tamura N., Masuzaki H., Mori K., Okazaki T.,
Satoh N., Shigemoto M., Yoshimasa Y., Nishi S., Hosada K., Inazawa J.,
Nakao K.;
RT "Structural organization and chromosomal assignment of the human obese gene."
RL J. Biol. Chem. 270:27728-27733(1995).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198511; PubMed=8621021;

RA Niki T., Mori H., Tamori Y., Kishimoto-Hashiramoto M., Ueno H.,
RA Araki S., Masugi J., Sawant N., Majithia H.R., Rais N.,
RA Hashiramoto M., Taniguchi H., Kasuga M.;
RT "Human obese gene: molecular screening in Japanese and Asian Indian
RT NIDDM patients associated with obesity.";
RL Diabetes 45:675-678(1996).
RN [8]
RP SEQUENCE FROM N.A.
RP Lu L., Fu Z., Xu M., Fu Y., Hu Z.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP INTERACTION WITH SIGLEC6.
RX MEDLINE=99357812; PubMed=10428856; DOI=10.1074/jbc.274.32.22729;
RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.;
RT "OB-BP1/Siglec-6. A leptin- and sialic acid-binding protein of the
RT immunoglobulin superfamily.";
RL J. Biol. Chem. 274:22729-22738(1999).
RN [11]
RP ERRATUM.
RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.;
RL J. Biol. Chem. 274:28058-28058(1999).
RN [12]
RP STRUCTURE BY NMR.
RX MEDLINE=97309492; PubMed=9166907; DOI=10.1016/S0014-5793(97)00353-0;
RA Kline A.D., Becker G.W., Churgay L.M., Landen B.E., Martin D.K.,
RA Muth W.L., Rathnachalam R., Richardson J.M., Schoner B., Ulmer M.,
RA Hale J.E.;
RT "Leptin is a four-helix bundle: secondary structure by NMR.";
RL FEBS Lett. 407:239-242(1997).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=97289390; PubMed=9144295.
RA Zhang F., Basinski M.B., Beale J.M., Briggs S.L., Churgay L.M.,
RA Clawson D.K., Dimarchi R.D., Furman T.C., Hale J.E., Hsiung H.M.,
RA Schoner B.E., Smith D.P., Zhang X.Y., Wery J.P., Schevitz R.W.;
RT "Crystal structure of the obese protein leptin-E100.";
RN Nature 387:206-209(1997).
RN [14]
RP VARIANT MET-94.
RA Bartholomew D.W., McClellan J.M.;
RT "A novel polymorphism in the leptin gene.";
RL Hum. Mutat. 12:220-220(1998).
RN [15]
RP VARIANT MORBID OBESITY TRP-105.
RX MEDLINE=98160176; PubMed=9500540;

RA Strobel A., Issa T., Camoin L., Ozata M., Strosberg A.D.;
RT "A leptin missense mutation associated with hypogonadism and morbid
RT obesity.";
RL Nat. Genet. 18:213-215(1998).
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -1- SUBUNIT: Interacts with SIGLEC6.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: Defects in LEP may be a cause of autosomal recessive
CC obesity [MIM:601665].
CC -1- SIMILARITY: Belongs to the leptin family.
CC -1- DATABASE: NAME=R&D Systems' cytokine mini-reviews: LEP;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=213".
CC -----
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CC -----
CC EMBL; U18915; AAA60470.1; -;
CC EMBL; D49487; BAA08448.1; -;
CC EMBL; U43653; AAC50400.1; -;
CC EMBL; U43415; AAC31660.1; -;
CC EMBL; D63710; BAA09839.1; -;
CC EMBL; D63709; BAA09839.1; JOINED.
CC EMBL; D63519; BAA09787.1; -;
CC EMBL; D63518; BAA09787.1; JOINED.
CC EMBL; AF008123; AAB63507.1; -;
CC EMBL; BC060830; AAB60830.1; -;
CC PIR; A38952; LTHU.
CC PIR; I53166; I53166.
CC PDB; 1AX8; X-ray; @=22-167.
CC Genew; HGNC:6553; LEP.
CC MIM; 164160; -;
CC MIM; 601665; -;
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0006112; P:energy reserve metabolism; TAS.
CC InterPro; IPR009079; 4_helix_cytokine.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC 3D-structure; Diabetes mellitus; Disease mutation; Obesity;
CC Polymorphism; Signal.
CC SIGNAL 1 21 Potential.
CC CHAIN 22 167 Leptin.
CC DISULFID 117 167
CC VARIANT 49 49 Missing (in 30% the clones).
CC
CC VARIANT 94 94 V -> M.
CC
CC VARIANT 105 105 /FTid=VAR_004196.
CC
CC VARIANT 110 110 /FTid=VAR_004197.
CC
CC VARIANT 110 110 R -> W (in morbid obesity and
CC hypogonadism).
CC
CC VARIANT 110 110 /FTid=VAR_008094.
CC
CC VARIANT 110 110 V -> M (in dbSNP:1800564).
CC
CC VARIANT 110 110 /FTid=VAR_011955.
CC
CC VARIANT 110 110 Q -> R (in Ref. 8).
CC
CC CONFLICT 96 96
CC HELIX 25 44
CC HELIX 72 87
CC TURN 88 88
CC TURN 92 114
CC TURN 115 116
CC TURN 128 131
CC HELIX 132 135
CC STRAND 137 137
CC TURN 138 139
CC STRAND 140 140

Query Match 99.5%; Score 866; DB 2; Length 167;
 Best Local Similarity 99.4%; Pred. No. 2.1e-70;
 Matches 166; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHWGTLGGFLWLPYLYVQAQVPIQKVQDDTKTLIKTIIVTRINDISHTSQVSSKKQVTGL 60
 DB 1 MHWGTLGGFLWLPYLYVQAQVPIQKVQDDTKTLIKTIIVTRINDISHTSQVSSKKQVTGL 60

QY 61 DFIPGLHPILTLTKMDQTLAVYQOILTSMPNRVQIISNDLENRLDLHLVAFSKSCHLP 120
 DB 61 DFIPGLHPILTLTKMDQTLAVYQOILTSMPNRVQIISNDLENRLDLHLVAFSKSCHLP 120

QY 121 WASGLTSLGSLGVLEASGYSTEVVALSRQGLQDLMLWOLDLSPGC 167
 DB 121 WASGLTSLGSLGVLEASGYSTEVVALSRQGLQDLMLWOLDLSPGC 167

RESULT 3

OB_MACMU STANDARD; PRT; 167 AA.

ID OB MACMU Q28504;
 AC Q28504;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonym=OB;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_TaxID=9544;
 [1]
 RP SEQUENCE FROM N.A.
 RN TISSUE=adipose tissue;
 RC MEDLINE=96411743; PubMed=8810296; DOI=10.1074/jbc.271.41.25327;
 RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Nicolson M.A.,
 RA Hansen B.C.;
 RA "Regulation of obese (ob) mRNA and plasma leptin levels in rhesus
 RT monkeys. Effects of insulin, body weight, and non-insulin-dependent
 RT diabetes mellitus";
 RL J. Biol. Chem. 271:25327-25331(1996).

CC -1- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: Belongs to the leptin family.

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 DR EMBL; U58492; AAC50730.1; --
 DR HSSP; P41159; IAX8.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000065; Leptin.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 DR Obesity; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 FT SEQUENCE 167 AA; 19953 MW; E7D9P30628A5BBE9 CRC64;

Query Match 89.7%; Score 780; DB 1; Length 167;
 Best Local Similarity 89.8%; Pred. No. 1.3e-62;

Matches 150; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MHWCTLCGFLWLPVLFVQAVPIQKQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MYWRTLMGFLWLPVLFYIQAVPIQKQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTSLKMDQTLAVYQIQLTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLP 120
Db 61 DFIPGLHPILTSLKMDQTLAVYQIQLTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLP 120
QY 121 WASGLETLDLSGGVLEASGYTEVVALSRQGSLODMWLQDLSPGC 167
Db 121 LASGLETLDLSGGVLEASGYTEVVALSRQGSLODMWLQDLSPGC 167
```

RESULT 4

```
OB_PANTR
ID OB_PANTR STANDARD; PRT; 146 AA.
AC O02750;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RA Rockey P.K., Rostock P.R.;
RT "Cloning of obese genes from different species: a comparison of the
RT gene structures and the sequences of the obese gene products,
RT leptin."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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```

```
EMBL; U96450; AB54023.1; -.
DR HSP; P41159; IAX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID
SQ SEQUENCE 146 AA; 16058 MW; 02C42A06B554D55C CRC64;
```

Query Match 84.3%; Score 733; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.9e-58;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 22 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 81
Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 60
QY 82 YQIILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGY 141
```

```
Db 61 YQIILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGY 120
QY 142 TEVALSRQGSLODMWLQDLSPGC 167
Db 121 TEVALSRQGSLODMWLQDLSPGC 146
```

RESULT 5

```
OB_GORGO
ID OB_GORGO STANDARD; PRT; 146 AA.
AC Q95189;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.P., Zhang X., Hsiung H.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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```

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EMBL; U72872; AB17091.1; -.
DR HSP; P41159; IAX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID
SQ SEQUENCE 146 AA; 16031 MW; 02C43BF6B9A4C85C CRC64;
```

Query Match 83.7%; Score 728; DB 1; Length 146;
Best Local Similarity 98.6%; Pred. No. 5.4e-58;
Matches 144; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
QY 22 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 81
Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 60
QY 82 YQIILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGY 141
Db 61 YQIILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGY 120
QY 142 TEVALSRQGSLODMWLQDLSPGC 167
Db 121 TEVALSRQGSLODMWLQDLSPGC 146
```

RESULT 6

```
OB_FELCA
ID OB_FELCA STANDARD; PRT; 167 AA.
```

AC Q9N2C1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=White adipose tissue;
 RA Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
 RT "Molecular cloning of feline leptin cDNA."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC -----
 DR EMBL; AB041360; BAA95481.1; -.
 DR HSSP; P41159; 1AX8.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000065; Leptin.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 DR Obesity; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 FT DIULFID 117 167 By similarity.
 SQ SEQUENCE 167 AA; 18583 MW; 643720DBB0AB4B95 CRC64;

 Query Match 83.2%; Score 724; DB 1; Length 167;
 Best Local Similarity 85.4%; Pred. No. 1.5e-57;
 Matches 140; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
 Qy 4 GTLCGFLWLPYFYVQAVPIQKQVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFI 63
 Db 4 GPLCRFLWLPYLSYVEAPIRKQVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFI 63
 Qy 64 PGLHPILTLKMDQTLAVYQIILTSMPNSRVQISNDLENLRLHLVLAFAKSKCHLPWAS 123
 Db 64 PGLHPVLSLKMDDQLATYQIILTSMPNSRVQISNDLENLRLHLVLAFAKSKCHLPWAS 123
 Qy 124 GLETLDISGGVLEAGSGYTEVVALSRLOGSLQDMLWQLDLSPGC 167
 Db 124 GLETLDISGGVLEAGSGYTEVVALSRLOGSLQDMLWQLDLSPGC 167

 RESULT 7
 OB_PONPY
 ID OB_PONPY STANDARD; PRT; 146 AA.
 AC Q95234;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin (Obesity factor).
 GN Name=LEP; Synonyms=OB;
 OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
 RT "Cloning of obese genes from different species: a comparison of the
 RT gene structures and the sequences of the obese gene products,
 RT leptin."
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC -----
 DR EMBL; U72873; AAB17092.1; -.
 DR HSSP; P41159; 1AX8.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000065; Leptin.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 DR Obesity.
 FT DISULFID 96 146 By similarity.
 FT DIULFID 96 146 By similarity.
 SQ SEQUENCE 146 AA; 16195 MW; 3F50A13338FFDBD4 CRC64;

 Query Match 82.9%; Score 721; DB 1; Length 146;
 Best Local Similarity 97.3%; Pred. No. 2.3e-57;
 Matches 142; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 22 VPIQKVQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 81
 Db 1 VPIQKVQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
 Qy 82 YQIILTSMPNSRVQISNDLENLRLHLVLAFAKSKCHLPWASGLETLDLSGLVLEAGSGYS 141
 Db 61 YQIILTSMPNSRVQISNDLENLRLHLVLAFAKSKCHLPWASGLETLDLSGLVLEAGSGYS 120
 Qy 142 TEVVALSRLOGSLQDMLWQLDLSPGC 167
 Db 121 TEVVALSRLOGSLQDMLWQLDLSPGC 146

 RESULT 8
 OB_PIG
 ID OB_PIG STANDARD; PRT; 167 AA.
 AC Q23406; O19095; Q95251;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB, OBS;
 OS Sus scrofa (Fig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adipose tissue;
 RA Louis C.F.;

RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ramsay T.G., Yan X.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace;
 RA Robert C., Palin M.-F., Coulombe N., Roberge C., Silversides F.G.,
 RA Benkel B.F., McKay R.M., Pelletier G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Bidwell C.A., Ji S., Spurlock M.E.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Meishan;
 RA Dai R., Li N., Hu X., Wu C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA McNeel R.L., Merzmann H.J.;
 RT "Adipose tissue regulatory transcript expression in lean versus obese
 RT pigs.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Large white;
 RA Soares M.A.M., Euclydes R.F., Guimaraes S.E.F., Martins M.P.,
 RA Lopes P.S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 15-110 FROM N.A.
 RC TISSUE=White adipose tissue;
 RX MEDLINE=97009821; PubMed=8856925;
 RA Neuenchwander S., Kettenberger G., Meijerink E., Jorg H.,
 RA Stranzinger G.;
 RT "Partial characterization of porcine obesity gene (OBS) and its
 RT localization to chromosome 18 by somatic cell hybrids.";
 RL Anim. Genet. 27:275-278(1996).
 CC -1- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC -----
 DR EMBL; U63540; AAB05923.1; -;
 DR EMBL; U59894; AAB03458.1; -;
 DR EMBL; AF026976; AAB82724.1; -;
 DR EMBL; U66254; AAB97308.1; -;
 DR EMBL; AF052691; AAC06303.1; -;
 DR EMBL; AF102856; AAC78147.1; -;
 DR EMBL; AF477387; AAL84792.1; -;
 DR EMBL; AF477386; AAL84792.1; JOINED.
 DR EMBL; U40812; AAC48641.1; -;
 DR HSPF; P41159; IAX8.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000065; Leptin.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 KW Obesity; Signal.

FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 FT CONFLICT 21 22 AV -> GP (in Ref. 8).
 FT CONFLICT 97 97 I -> L (in Ref. 8).
 FT CONFLICT 122 122 A -> R (in Ref. 4).
 SQ SEQUENCE 167 AA; 18661 MW; 27550E1E0E63814E CRC64;
 Query Match 82.2%; Score 715; DB 1; Length 167;
 Best Local Similarity 85.0%; Pred. No. 9.7e-57;
 Matches 142; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
 Oy 1 MHNGTLCGFLWLPYLFYQAVPIQYQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60
 Db 1 MRCGPLCRFLWLPYLSYVEAVPIRWYQDDTKTIKTIIVTRISDISHMQSVSSKQKVTGL 60
 Oy 61 DFTPLHPIILTSKMDQTLAVYQIILTSMPNRVQISNDLENLRDLHLVAFKSKCHLP 120
 Db 61 DFTPLHPIILTSKMDQTLAVYQIILTSMPNRVQISNDLENLRDLHLVAFKSKCHLP 120
 Oy 121 WASGLETLDSIGGVLEASGYSTEVVALSRQGSLODMLWOLDLSPGC 167
 Db 121 QARALETLSLGGVLEASLYSTEVVALSRQGSLODMLWOLDLSPGC 167
 RESULT 9
 OB_BOVIN STANDARD; PRT; 167 AA.
 AC P50595; Q97918; Q95133; Q9TS29;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB, OBS;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 CX NCBI_TaxID=9913;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Tellam R.L., Briscoe S., Vuocolo A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 22-167 FROM N.A.
 RA Ji S., Spurlock M.E.;
 RT "Partial cloning of bovine obesity gene.";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE OF 22-167 FROM N.A.
 RC TISSUE=White adipose tissue;
 RA Kawakita Y., Abe H., Miyashige T.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A., AND VARIANTS CYS-25 AND VAL-80.
 RC STRAIN=Jersey;
 RX MEDLINE=20063685; PubMed=10594237;
 RA Konfortov B.A., Licence V.E., Miller J.R.;
 RT "Resequencing of DNA from a diverse panel of cattle reveals a high
 RT level of polymorphism in both intron and exon.";
 RL Mamm. Genome 10:1142-1145(1999).
 [5]
 RP SEQUENCE FROM N.A., AND VARIANT CYS-25.
 RA Liefers S.C.;
 RT "Genotype effects of bovine leptin mutations on pre- and postpartum
 RT leptin concentrations.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 [6]
 RP SEQUENCE OF 46-145 FROM N.A.
 RA Lien S., Sundvold H., Klungland H., Vaage D.I.;
 RT "Two novel polymorphisms in the bovine obesity gene (OBS).";
 RL Anim. Genet. 28:245-245(1997).

```

[7]
RN  SEQUENCE OF 60-146 FROM N.A.
RX  MEDLINE=96269621; PubMed=8661738;
RT  Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.;
RA  "Chromosomal localization of the bovine obesity (OBS) gene.";
RL  Mamm. Genome 7:398-399(1996).
[8]
RN  SEQUENCE OF 1-48 FROM N.A.
RA  Fitzsimmons C.J., Schmutz S.M.;
RT  Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL  "Exon two of the bovine obese, leptin, gene.";
CC  -1- FUNCTION: May function as part of a signaling pathway that acts to
CC  regulate the size of the body fat depot. An increase in the level
CC  of LEP may act directly or indirectly on the CNS to inhibit food
CC  intake and/or regulate energy expenditure as part of a homeostatic
CC  mechanism to maintain constancy of the adipose mass.
CC  -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC  -1- SIMILARITY: Belongs to the leptin family.
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-----
DR  EMBL; U43943; AA85906.1; -.
DR  EMBL; U50365; AAB61244.1; -.
DR  EMBL; U65793; AAB06579.1; -.
DR  EMBL; AB003143; BAA19750.1; -.
DR  EMBL; AJ132764; CAB84235.1; -.
DR  EMBL; AJ236854; CAB38018.1; -.
DR  EMBL; AJ512638; CAD54745.1; -.
DR  EMBL; AJ512639; CAD54745.1; JOINED.
DR  EMBL; Y11369; CAA72197.1; -.
DR  EMBL; U43833; AAB18762.1; -.
DR  EMBL; AF120500; AAD23567.1; -.
DR  HSSP; P41159; IAX8.
DR  InterPro; IPR009079; 4_helix_cytokine.
DR  InterPro; IPR000065; Leptin.
DR  Pfam; PF02024; Leptin; 1.
DR  PRINTS; PR00495; LEPTIN.
DR  ProDom; PD005698; Leptin; 1.
KW  Obesity; Polymorphism; Signal.
FT  SIGNAL 1 21 Potential.
FT  CHAIN 22 167 Leptin.
FT  DISULFID 117 167 By similarity.
FT  VARIANT 25 25 R -> C.
FT  VARIANT 80 80 A -> V.
FT  CONFLICT 25 25 R -> Q (in Ref. 2).
FT  CONFLICT 166 166 G -> E (in Ref. 2).
SQ  SEQUENCE 167 AA; 18716 MW; 94C666B3069E50B7 CRC64;

Query Match 81.0%; Score 705; DB 1; Length 167;
Best Local Similarity 84.4%; Pred. No. 7.8e-56;
Matches 141; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 MHWTGTCGFLWLPVLYVQVPIQKVQDDTKTLIKTVTRINDISHTQSVSSKQVKTGL 60
DB 1 MRCGLPFLWLPVLYSVLVEAPVPIKQVQDDTKTLIKTVTRINDISHTQSVSSKQVKTGL 60

QY 61 DFIPLGLPILTSKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLP 120
DB 61 DFIPLGLPILLSKMDQTLAIYQQILTSLSRNVVQISNDLENLRLDLHLVAFSKSCHLP 120

QY 121 WASGLTDLSDGLGVLEASGYSTEVVALSRQGSLODMLWQDLSPGC 167
DB 121 QVRALESLESGLVLEASLYSTEVVALSRQGSLODMLRQLDLSFGC 167

RESULT 10
OB_MOUSE STANDARD; PRT; 167 AA.
P41160;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leptin precursor (Obesity factor).
Name=lep; Synonyms=Ob;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;
RA  Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RT  "Positional cloning of the mouse obese gene and its human homologue.";
RL  Nature 372:425-432(1994).
[2]
RN  ERRATUM.
RA  Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RL  Nature 374:479-479(1995).
[3]
RN  SEQUENCE FROM N.A.
RA  Chehab F.F., Lim M.E.;
RT  Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RL  -1- FUNCTION: May function as part of a signaling pathway that acts to
RL  regulate the size of the body fat depot. An increase in the level
RL  of Lep may act directly or indirectly on the CNS to inhibit food
RL  intake and/or regulate energy expenditure as part of a homeostatic
RL  mechanism to maintain constancy of the adipose mass.
RL  -1- SUBCELLULAR LOCATION: Secreted (Probable).
RL  -1- DISEASE: Defects in Lep are the cause of profound obesity and type
RL  II diabetes.
RL  -1- SIMILARITY: Belongs to the leptin family.
-----
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL; U18812; AAA64564.1; -.
DR  EMBL; U22421; AAA64213.1; -.
DR  PIR; S50863; LTMS.
DR  HSSP; P41159; IAX8.
DR  MGD; MGI:104663; Lep.
DR  GO; GO:0008083; F:growth factor activity; IDA.
DR  GO; GO:0005515; F:protein binding; IPI.
DR  GO; GO:0008206; P:bile acid metabolism; IDA.
DR  GO; GO:0045639; P:positive regulation of myeloid blood cell d. . ; IDA.
DR  GO; GO:0030300; P:regulation of cholesterol absorption; IDA.
DR  InterPro; IPR009079; 4_helix_cytokine.
DR  InterPro; IPR000065; Leptin.
DR  Pfam; PF02024; Leptin; 1.
DR  PRINTS; PR00495; LEPTIN.
DR  ProDom; PD005698; Leptin; 1.
KW  Diabetes mellitus; Obesity; Signal.
FT  SIGNAL 1 21 Potential.
FT  CHAIN 22 167 Leptin.
FT  DISULFID 117 167 By similarity.
FT  VARIANT 49 49 Missing (in 30% the clones).
SQ  SEQUENCE 167 AA; 18708 MW; D67836C76FD7116 CRC64;

Query Match 80.9%; Score 704; DB 1; Length 167;
Best Local Similarity 83.2%; Pred. No. 9.6e-56;
Matches 139; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MHWTGTCGFLWLPVLYVQVPIQKVQDDTKTLIKTVTRINDISHTQSVSSKQVKTGL 60
DB 1 MCRPLCFLWLSYLSVQVPIQKVQDDTKTLIKTVTRINDISHTQSVSAKQVKTGL 60
```

```

OY 61 DFIPGLHPILTSLKMDOTLAVYQOILTSMPNRNVIQISNDLENLRLDHLHLAFSKSCHLP 120
DB 61 DFIPGLHPILSLKMDOTLAVYQOILTSMPNRNVIQISNDLENLRLDHLHLAFSKSCHLP 120

OY 121 WASGLETLDLSDGLVLEASGYSTEVVALSRLOGLSLQDMLWQLDLSGPC 167
DB 121 QTSGLQKPESLDGLVLEASLYSTEVVALSRLOGLSLQDILQLDLSPEC 167

RESULT 11
OB_RAT OB_RAT STANDARD; PRT; 167 AA.
AC P50596;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=lep; Synonyms=Ob;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=95386724; PubMed=7657834;
RA Ogawa Y., Masuzaki H., Isse N., Okazaki T., Mori K., Shigemoto M.,
RA Satoh N., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,
RA Nakao K.;
RT "Molecular cloning of rat obese cDNA and augmented gene expression in
RT genetically obese Zucker fatty (fa/fa) rats.";
RL J. Clin. Invest. 96:1647-1652(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Fat;
RX MEDLINE=95314614; PubMed=7794258;
RA Funahashi T., Shimomura I., Hiraoka H., Arai T., Takahashi M.,
RA Nakamura T., Nozaki S., Yamashita S., Takemura K., Tokunaga K.;
RT "Enhanced expression of rat obese (ob) gene in adipose tissues of
RT ventromedial hypothalamus (VMH)-lesioned rats";
RL Biochem. Biophys. Res. Commun. 211:469-475(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Leto, Oletf, and Zucker; TISSUE=Adipose tissue;
RX MEDLINE=95251725; PubMed=7733988;
RA Murakami T., Shima K.;
RT "Cloning of rat obese cDNA and its expression in obese rats.";
RL Biochem. Biophys. Res. Commun. 209:944-952(1995).
RN [4]
RP SEQUENCE OF 14-167 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Fat;
RA Donohue P.A., Sivitz W.I., Bailey H.L.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of Lep may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; D45862; BAA08296.1; -
DB EMBL; S78586; AAB34657.2; -
DB EMBL; D49653; BAA08529.1; -

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DR EMBL; U49849; AAC52514.1; -
DR PIR; PC4034; LTRT.
DR HSP; P41159; IAX8.
DR RGD; 3000; Lep.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT CONFLICT 32 32 K -> T (in Ref. 2).
FT CONFLICT 163 163 L -> V (in Ref. 4).
SQ SEQUENCE 167 AA; 18866 MW; 3B5B563DA42EC4E CRC64;

Query Match 79.3%; Score 690; DB 1; Length 167;
Best Local Similarity 82.0%; Pred. No. 1.8e-54;
Matches 137; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

OY 1 MHWGTLGFLWPELYFVQAVPIQKVDOTKTLIKTIVTRINDISHTQSVSSKQVTGL 60
DB 1 MCWRPLCRFLWLSYLSYQAVPIHKVDDTKTLIKTIVTRINDISHTQSVSARQRTGL 60.

OY 61 DFIPGLHPILTSLKMDOTLAVYQOILTSMPNRNVIQISNDLENLRLDHLHLAFSKSCHLP 120
DB 61 DFIPGLHPILSLKMDOTLAVYQOILTSMPNRNVIQISNDLENLRLDHLHLAFSKSCHLP 120

OY 121 WASGLETLDLSDGLVLEASGYSTEVVALSRLOGLSLQDMLWQLDLSGPC 167
DB 121 QTSGLQKPESLDGLVLEASLYSTEVVALSRLOGLSLQDILQLDLSPEC 167

RESULT 12
OB_CANFA OB_CANFA STANDARD; PRT; 167 AA.
AC O02720; Q9TSG1;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=White adipose tissue;
RA Iwase M., Sasaki N., Komagome R., Kimura K., Saito M.;
RT "Molecular cloning of canine leptin cDNA.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 22-167 FROM N.A.
RC TISSUE=Adipose tissue;
RA Smith D.P., Zhang X., Hsiung H.M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC -----
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Qy 22 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
Db 1 VPIRKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAI 60
Qy 82 YQQLTSPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 141
Db 61 YQQLTSPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Qy 142 TEVVALSRLOGLQDMLWQLDLSFGC 167
Db 121 TEVVALSRLOGLQDMLRQLDLSFGC 146

RESULT 15

OB SHEEP
ID OB SHEEP STANDARD; PRT; 146 AA.
AC Q28603; P79212;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN (1)
RN SEQUENCE FROM N.A.
RN TISSUE=Adipose tissue;
RA Simmons J.M., Dyer C.J., Keisler D.H.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN (2)
RN SEQUENCE OF 9-125 FROM N.A.
RN TISSUE=Adipose tissue;
RX MEDLINE=98006799; PubMed=9347250; DOI=10.1016/S0739-7240(97)00028-3;
RA Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.;
RT "cDNA cloning and tissue-specific gene expression of ovine leptin,
RL NPY-Y1 receptor, and NPY-Y2 receptor."
RL Domest. Anim. Endocrinol. 14:295-303(1997).
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U84247; AAB41786.1; -;
DR EMBL; U62123; AAB51033.1; -;
DR HSPSP; P41159; IAX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
FT CONFLICT 65 65 L -> H (in Ref. 2).
FT CONFLICT 92 92 A -> G (in Ref. 2).
FT CONFLICT 124 124 V -> L (in Ref. 2).
SQ SEQUENCE 146 AA; 16053 MW; 19D54C53240968CA CRC64;
Query Match 71.7%; Score 624; DB 1; Length 146;
Best Local Similarity 87.0%; Pred. No. 1.4e-48;

Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
Qy 22 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
Db 1 VPIRKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAI 60
Qy 82 YQQLTSPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 141
Db 61 YQQLTSPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Qy 142 TEVVALSRLOGLQDMLWQLDLSFGC 167
Db 121 TEVVALSRLOGLQDMLRQLDLSFGC 146

Search completed: March 12, 2005, 05:03:38
Job time : 122.581 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:44:03 ; Search time 109.15 Seconds
(without alignments)
517.333 Million cell updates/sec

Title: US-10-049-182-6
Perfect score: 736
Sequence: 1 VPIQKVQDPTXLTIKTIVTR.....SRLOGLQDMLWQLDLSPGC 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736	100.0	146	2 AAW00013	Acid stab
2	736	100.0	146	2 AAR99490	Chimeric
3	736	100.0	146	2 AAW00539	Human mat
4	736	100.0	146	2 AAW30892	Synthetic
5	736	100.0	146	2 AAW34482	Human obe
6	736	100.0	146	2 AAW10151	Properly
7	736	100.0	146	2 AAW22901	Biologica
8	736	100.0	146	2 AAW30791	Obesity p
9	736	100.0	146	2 AAW26194	Obesity p
10	736	100.0	146	2 AAW34483	Human obe
11	736	100.0	146	2 AAW32575	Anti obes
12	736	100.0	146	2 AAW34489	Obesity p
13	736	100.0	146	2 AAW69682	Human obe
14	736	100.0	146	2 AAW53342	Obesity p
15	736	100.0	146	2 AAY43311	Human lep
16	736	100.0	146	2 AAY06102	Human obe
17	736	100.0	146	3 AAY92712	Mature le
18	736	100.0	146	3 AAY82111	Mature hu
19	736	100.0	146	3 AAY80260	Human mat
20	736	100.0	146	3 AAY83768	Human OB
21	736	100.0	146	3 AAY97871	Mature wi
22	736	100.0	146	3 AAY95786	Mature re
23	736	100.0	146	3 AAY95531	Human mat
24	736	100.0	146	3 AAB14265	Mature hu
25	736	100.0	146	4 AAB70130	Mature hu

26	736	100.0	146	5 AAE23614	Human lep
27	736	100.0	146	5 ABG32264	Recombina
28	736	100.0	146	5 ABP63579	Human obe
29	736	100.0	146	5 ADG65529	Human lep
30	736	100.0	146	5 ABR57162	Recombina
31	736	100.0	146	7 ADC06694	Leptin ta
32	736	100.0	146	7 ADD26675	Human adi
33	736	100.0	146	7 ADD71107	Human lep
34	736	100.0	146	8 ADL80474	Mature hu
35	736	100.0	146	8 ADL88877	Human cyt
36	736	100.0	147	2 AAW34394	Human Met
37	736	100.0	147	2 AAW27167	Human rsc
38	736	100.0	147	2 AAW53328	Human obe
39	736	100.0	147	2 AAY43314	Human lep
40	736	100.0	147	3 AAY92261	Mature re
41	736	100.0	148	2 AAW07192	Human ant
42	736	100.0	148	2 AAW28801	Human mas
43	736	100.0	148	2 AAW71849	Obesity p
44	736	100.0	166	2 AAW00535	Human obe
45	736	100.0	167	2 AAW03694	Human obe

ALIGNMENTS

RESULT 1
AAW00013
ID AAW00013 standard; protein; 146 AA.
XX
AC AAW00013;
XX
DT 30-SEP-1996 (first entry)
XX
DE Acid stable modified ob protein (Asp22Asn).
XX
KW ob protein; adiposity regulating hormone; mouse; acid stability;
KW adsorption characteristic; obesity; type II diabetes;
KW cardiovascular disease; cancer.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 22 /Label= Asp22Asn
FT Disulfide-bond 96. .146
XX
PN EP725078-Al.
XX
PD 07-AUG-1996.
XX
PF 29-JAN-1996; 96EP-00300612.
XX
PR 31-JAN-1995; 95US-00381048.
PR 06-FEB-1995; 95US-00383638.
XX
(ELIL) LILLY & CO ELI.
XX
PI Basinsky MB, Dimarchi RD, Heath WF, Schoner BE;
XX
DR WPI; 1996-356062/36.
XX
Mammalian derived anti-obesity proteins which regulate fat tissue - used for treating obesity and to reduce risk for type II diabetes, cardiovascular disease and cancer.
XX
Example 4; Page 19; 42pp; English.
XX
This sequence represents a modified ob proteins. ob proteins are thought to be adiposity regulating hormones. This sequence is based on the mouse ob protein sequence. Proteins such as this have improved stability, esp. acid stability, and improved adsorption characteristics compared to the wild type protein disclosed in Yiyang Zhang et al, Nature 372: 425-32 (December 1994). These proteins correspond to the generic formulae given

CC in AAR99497-98). They are biologically active for the treatment of
CC obesity. Individuals treated with these proteins have a reduced risk for
CC type II diabetes, cardiovascular disease and cancer
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSMPNRVNIQISNDLENLRLHVLAFSKSCHLPWASGLTDLGLGVLEASGYS 120
DB 61 YQOILTSMPNRVNIQISNDLENLRLHVLAFSKSCHLPWASGLTDLGLGVLEASGYS 120
QY 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146
DB 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 2
AAR99490
ID AAR99490 standard; protein; 146 AA.
XX
AC AAR99490;

DT 16-OCT-2003 (revised)
DT 26-SEP-1996 (first entry)
XX

XX Chimeric ob protein.

XX ob protein; human; substitution; murine; mouse; obesity; stability;
KW type II diabetes; cardiovascular disease; cancer.
XX

OS Mus musculus.
OS Homo sapiens.
OS Chimeric.

PH Key Location/Qualifiers
FT Misc-difference 22 /note= "Opt. Gln or Asp"
FT Misc-difference 27 /note= "Opt. Ala"
FT Misc-difference 28 /note= "Opt. Glu or absent"
FT Misc-difference 54 /note= "Opt. Ala"
FT Misc-difference 68 /note= "Opt. Leu"
FT Misc-difference 72 /note= "Opt. Glu or Asp"
FT Misc-difference 77 /note= "Opt. Ala"
FT Disulfide-bond 96.146
FT Misc-difference 97

FT /note= "Opt. replaced with Gln, Asn, Ala, Gly, Ser or
FT Misc-difference 100
FT /note= "Opt. replaced with Ala, Glu, Asp, Asn, Met, Ile,
FT Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT Misc-difference 101 /note= "Opt. replaced with Ser, Asn, Gly, His, Pro, Thr
FT or Val"
FT Misc-difference 102 /note= "Opt. replaced with Arg"
FT Misc-difference 103 /note= "Opt. replaced with Ala"
FT Misc-difference 105 /note= "Opt. replaced with Gln"
FT Misc-difference 106

FT Misc-difference 107 /note= "Opt. replaced with Lys or Ser"
FT Misc-difference 108 /note= "Opt. replaced with Pro"
FT Misc-difference 111 /note= "Opt. replaced with Glu"
FT Misc-difference 118 /note= "Opt. replaced with Asp"
FT Misc-difference 138 /note= "Opt. Leu"
FT /note= "Opt. replaced with Ala, Glu, Asp, Asn, Met, Ile,
FT Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
XX

PN EP725079-A1.

PD 07-AUG-1996.

XX 29-JAN-1996; 96EP-00300613.

PR 31-JAN-1995; 95US-00381048.

PR 06-FEB-1995; 95US-00383638.

PR 22-JUN-1995; 95US-0000450P.

PR 11-AUG-1995; 95US-0002161P.

XX (ELIL) LILLY & CO ELI.

XX Basinski MB, Dimarchi RD, Flora DB, Hale JE, Heath WF;

PI Hoffmann JA, Schoner BE;

XX WPI; 1996-356063/36.

DR N-PSDB; AAT34254.

XX Modified human anti-obesity proteins which regulate fat tissue - have
XX increased stability, for treating obesity and to reduce risk for type II
XX diabetes, cardiovascular disease and cancer.

XX Claim 3; Page 47; 56pp; English.

XX The sequences given in AAR99490-96 represent modified ob proteins which
XX are based on the human ob protein sequence. These protein sequences are
XX covered by the generic sequence given in AAR99489. In these proteins,
XX specific amino acids are substituted for the residues found in the
XX corresponding positions in murine ob protein. These proteins are
XX biologically active for the treatment of obesity, and are more stable
XX than either the murine or human proteins. Individuals treated with these
XX proteins have a reduced risk for type II diabetes, cardiovascular disease
XX and cancer. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPNRVNIQISNDLENLRLHVLAFSKSCHLPWASGLTDLGLGVLEASGYS 120
DB 61 YQOILTSMPNRVNIQISNDLENLRLHVLAFSKSCHLPWASGLTDLGLGVLEASGYS 120
QY 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146
DB 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 3
AAW00539

ID AAW00539 standard; protein; 146 AA.

XX AC AAW00539;

XX

```
DT 13-SEP-1996 (first entry)
XX Human mature obesity protein.
XX
XX Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
XX food intake; energy expenditure; high blood pressure; cholesterol; human;
XX Gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
XX Homo sapiens.
XX OS
XX GB2292382-A.
XX PN
XX 21-FEB-1996.
XX PD
XX 17-AUG-1995; 95GB-00016947.
XX PF
XX 17-AUG-1994; 94US-00292345.
XX PR
XX 30-NOV-1994; 94US-00347563.
XX PR
XX 10-MAY-1995; 95US-00438431.
XX PR
XX 07-JUN-1995; 95US-00483211.
XX PR
XX (UVRQ) UNIV ROCKEFELLER.
XX PA
XX Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
XX Burley SK;
XX PI
XX WPI; 1996-099009/11.
XX DR
XX Obesity polypeptide(a) able to modulate body wt. - useful for e.g.
XX reducing wt. in treatment of diabetes, high blood pressure and high
XX cholesterol and for cosmetic reasons.
XX PT
XX Claim 11; Page ?; 304pp; English.
XX PS
XX AAW00538-W00541 represent the mature proteins of the murine and human
XX obesity polypeptides (OBP) (full length sequences represented by AAR92719
XX and AAR92720). OBP (also known as leptin) is a hormone involved in the
XX regulation of body weight. This sequence has effects on both food intake
XX and energy expenditure. OBP and its analogues are useful for modifying
XX body weight (optionally combined with known medicaments), for treating
XX diabetes, high blood pressure or high cholesterol. The DNA encoding this
XX sequence (and sequences complementary to it) can be used in gene therapy
XX for modifying body weight. This protein can be used for reducing weight
XX for health or cosmetic reasons in obese humans, or to produce leaner food
XX animals. Antagonists of OBP (including antibodies) are useful for
XX increasing body weight, e.g. for treating weight loss associated with
XX cancer, or for cosmetic reasons in humans, or for production of Kobe beef
XX or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in
XX diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP
XX complexes enables in vitro evaluation of levels of OBP in a sample,
XX especially to detect diseases associated with elevated or decreased
XX levels, and to monitor treatment of these diseases
XX SQ
XX Sequence 146 AA;
XX
XX Query Match 100.0%; Score 736; DB 2; Length 146;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-73;
XX Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLTKMDQTLAV 60
XX DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLTKMDQTLAV 60
XX
XX QY 61 YQOILTSMPSNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
XX DB 61 YQOILTSMPSNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
XX
XX QY 121 TEVVALSRLOGLQSLQDMLWQLDLSGPC 146
XX DB 121 TEVVALSRLOGLQSLQDMLWQLDLSGPC 146
XX
XX RESULT 5
XX AAW34482
XX ID AAW34482 standard; protein; 146 AA.
XX AC AAW34482;
XX 17-MAR-1998 (first entry)
XX DT
XX Human obesity protein.
XX DE
XX Obesity protein; therapy; obesity associated disorder; human.
XX KW
XX Homo sapiens.
XX OS
```

RESULT 4

PN EP784979-A2.
 XX 23-JUL-1997.
 PD 17-JAN-1997; 97EP-00300299.
 PF 19-JAN-1996; 96US-0010229P.
 XX 07-FEB-1996; 96GB-00002408.
 XX (ELIL) LILLY & CO ELI.
 XX Beals JM, Dodd SW, Pekar AH;
 XX WPI; 1997-365736/34.
 DR New obesity protein compositions - comprising a soluble parenteral
 PT formulation containing a preservative selected from an alkyl:paraben and
 PT chlorobutanol.
 XX Disclosure; Page 6; 15pp; English.
 XX This sequence represents the human obesity protein. It can be used in the
 CC formulation of the invention. The formulation of the invention is a
 CC soluble parenteral formulation that comprises an obesity protein and a
 CC preservative selected from an alkylparaben, chlorobutanol, or a mixture.
 CC The compositions can be used for treating obesity and disorders
 CC associated with obesity. In the formulations, the obesity protein remains
 CC stable and soluble at much higher concentrations and at a pH range
 CC acceptable for a soluble, parenteral formulation
 XX Sequence 146 AA;
 SQ
 Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 7.8e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
 Db 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
 QY 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 Db 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 RESULT 6
 AAW10151
 ID AAW10151 standard; protein; 146 AA.
 XX AAW10151;
 AC 27-AUG-2003 (revised)
 DT 02-OCT-1997 (first entry)
 XX Properly folded obesity protein intermediate.
 DE Intermediate; recombinant; production; obesity; regulation; fatty tissue;
 KW treatment; disease; diabetes; cardiovascular; cancer; properly folded.
 XX Mammalia.
 OS
 XX Key Location/Qualifiers
 XX Modified-site 1
 FT /label= Val-R3
 FT /note= "R3 is absent, Met, Met-R4 or leader sequence
 FT (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW08589-94),
 FT and R4 is any amino acid other than Pro"
 FT Modified-site 96
 FT /note= "free Cys residue or part of mixed disulfide with,
 FT e.g. Cys, glutathione or 2-mercaptoethanol when Cys146 is
 FT free Cys residue"
 FT Modified-site 146
 FT /note= "free Cys residue or part of mixed disulfide with,
 FT e.g. Cys, glutathione or 2-mercaptoethanol when Cys96 is
 FT free Cys residue"
 PN W09700886-A1.
 XX 09-JAN-1997.
 PD 20-JUN-1996; 96WO-US010613.
 PF 22-JUN-1995; 95US-0000451P.
 XX (ELIL) LILLY & CO ELI.
 XX Hale JE, Mackellar W;
 XX WPI; 1997-087317/08.
 DR Properly folded intermediate for obesity protein - prep. from inclusion
 PT bodies, provides high yield of active protein for treatment of obesity
 PT and its complications.
 XX Claim 1; Page 21; 66pp; English.
 CC AAW10151 is a properly folded intermediate for the production of the
 CC biologically active obesity protein AAW22901, which has a similar
 CC structure but comprises a disulphide bridge between Cys96 and Cys146.
 CC AAW10151 is the final intermediate in the renaturation of a recombinant
 CC protein to AAW22901, which is an active anti-obesity protein for the
 CC regulation of fatty tissue and treatment of obesity related diseases,
 CC e.g. diabetes, cardiovascular disease and cancer. The production of
 CC AAW22901 via AAW10151 provides a high yield of active protein, and
 CC permits large scale manufacture with a high concentration of protein
 CC during the folding stage. AAW10151 already has the correct tertiary
 CC structure and conversion to AAW22901 is almost quantitative, with minimal
 CC formation of S-S linked dimers or multimers, negating the need for an
 CC aggregation preventing agent. AAW10151 is stable in the presence or
 CC absence of denaturant, is soluble in phosphate buffered saline and can be
 CC purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 146 AA;
 SQ
 Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 7.8e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
 Db 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
 QY 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 Db 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 RESULT 7
 AAW22901
 ID AAW22901 standard; protein; 146 AA.
 XX AAW22901;
 AC 27-AUG-2003 (revised)
 DT 02-OCT-1997 (first entry)
 XX Biologically active obesity protein.
 DE

KW Intermediate; recombinant; production; obesity; regulation; fatty tissue;
XX treatment; disease; diabetes; cardiovascular; cancer; properly folded.

OS Mammalia.

XX Key Location/Qualifiers
XX Modified-site 1

FT /label= Val-R3
FT /note= "R3 is absent, Met, Met-R4 or leader sequence
FT (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW08589-94),
FT and R4 is any amino acid other than Pro"
FT Disulfide-bond 96. 146

XX PN WO9700886-A1.

XX PD 09-JAN-1997.

XX PF 20-JUN-1996; 96WO-US010613.

XX PR 22-JUN-1995; 95US-0000451P.

XX PA (ELIL) LILLY & CO ELI.

XX PI Hale JE, Mackellar W;

XX WPI; 1997-087317/08.

XX Properly folded intermediate for obesity protein - prepd. from inclusion
PT bodies, provides high yield of active protein for treatment of obesity
PT and its complications.

PS Claim 12; Page 21; 66pp; English.

CC AAW10151 is a properly folded intermediate for the production of the
CC biologically active obesity protein AAW22901, which has a similar
CC structure but comprises a disulfide bridge between Cys96 and Cys146.
CC AAW10151 is the final intermediate in the renaturation of a recombinant
CC protein to AAW22901, which is an active anti-obesity protein for the
CC regulation of fatty tissue and treatment of obesity related diseases,
CC e.g. diabetes, cardiovascular disease and cancer. The production of
CC AAW22901 via AAW10151 provides a high yield of active protein, and
CC permits large scale manufacture with a high concentration of protein
CC during the folding stage. AAW10151 already has the correct tertiary
CC structure and conversion to AAW22901 is almost quantitative, with minimal
CC formation of S-S linked dimers or multimers, negating the need for an
CC aggregation preventing agent. AAW10151 is stable in the presence or
CC absence of denaturant, is soluble in phosphate buffered saline and can be
CC purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

Qy 61 YQOILTSMPSPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQOILTSMPSPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120

Qy 121 TEVALSRLOQSLQDMLWQLDLSFGC 146

Db 121 TEVALSRLOQSLQDMLWQLDLSFGC 146

RESULT 8

AAW30791

ID AAW30791 standard; protein; 146 AA.

XX AC AAW30791;

XX

DT 12-MAR-1998 (first entry)

XX Obesity protein complexed with a divalent metal cation.

XX DE Obesity protein; diabetes; cancer; cardiovascular disease;

XX KW divalent metal cation; leader sequence.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 96. 146

XX PN WO9728824-A1.

XX PD 14-AUG-1997.

XX PF 24-JAN-1997; 97WO-US001188.

XX PR 06-FEB-1996; 96US-0011238P.

XX PA (ELIL) LILLY & CO ELI.

XX PI Hoffmann JA;

XX WPI; 1997-415077/38.

XX New compound comprising obesity protein and divalent metal cation - for

PT treatment of obesity and associated conditions, required at lower dose

PT than free protein.

PS Claim 3; Page 26; 33pp; English.

CC The present sequence represents a human obesity protein, which is

CC complexed with a divalent metal cation e.g. zinc and optionally has a

CC leader sequence. It is used to treat obesity and conditions (particularly

CC type II diabetes, cardiovascular disease and cancer) associated with it.

CC When formulated with the metal ion, it is more active, allowing reduction

CC in dose and thus reduction in cost and toxic side effects

XX SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;

Best Local Similarity 100.0%; Pred. No. 7.8e-73;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

Qy 61 YQOILTSMPSPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120

Db 61 YQOILTSMPSPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120

Qy 121 TEVALSRLOQSLQDMLWQLDLSFGC 146

Db 121 TEVALSRLOQSLQDMLWQLDLSFGC 146

RESULT 9

AAW26194

ID AAW26194 standard; protein; 146 AA.

XX AC AAW26194;

XX DT 18-FEB-1998 (first entry)

XX DE Obesity protein analogue #6.

XX KW Obesity protein analogue; divalent metal cation complex; therapy; cancer;

XX obesity; obesity associated disorder; diabetes; cardiovascular disease.

XX OS Synthetic.

XX Key Location/Qualifiers
FH Disulfide-bond 96. .146
FT Misc-difference 97
FT /note= "optionally replaced with Gln, Asn, Ala, Gly, Ser
FT or Pro"
FT Misc-difference 100
FT /note= "optionally replaced with Ala, Glu, Asp, Asn, Met,
FT Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT Misc-difference 101
FT /note= "optionally replaced with Ser, Asn, Gly, His, Pro,
FT Thr or Val"
FT Misc-difference 102
FT /note= "optionally replaced with Arg"
FT Misc-difference 103
FT /note= "optionally replaced with Ala"
FT Misc-difference 105
FT /note= "optionally replaced with Gln"
FT Misc-difference 106
FT /note= "optionally replaced with Lys or Ser"
FT Misc-difference 107
FT /note= "optionally replaced with Pro"
FT Misc-difference 108
FT /note= "optionally replaced with Glu"
FT Misc-difference 111
FT /note= "optionally replaced with Asp"
FT Misc-difference 138
FT /note= "optionally replaced with Ala, Glu, Asp, Asn, Met,
FT Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
XX WO9726916-A1.
XX 31-JUL-1997.
XX 24-JAN-1997; 97WO-US001189.
XX 25-JAN-1996; 96US-0011055P.
XX (ELIL) LILLY & CO ELI.
XX Hoffmann JA;
XX WPI; 1997-393377/36.
XX Obesity protein analogue complexed with divalent metal cation - useful
XX for treating obesity and associated disorders, e.g. diabetes,
XX cardiovascular disease and cancer.
XX Disclosure; Page 11; 45pp; English.
XX AAW26190 and AAW26192-W26201 represent obesity protein
XX analogues contained in the compound of the invention. These sequences
XX were synthetically created from the sequence shown in AAW26191. The
XX compound of the invention comprises one of these obesity protein
XX analogues complexed with a divalent metal cation (preferably Zn⁺⁺). The
XX specification does not indicate where the divalent metal cation complexes
XX to on the obesity protein analogue. The compound of the invention (or a
XX parenteral pharmaceutical formulation containing it) can be used to treat
XX obesity. It may also be used to treat disorders associated with obesity
XX such as diabetes, cardiovascular disease and cancer. The compound allows
XX effective pharmacological treatment at lower doses than significantly
XX reduce the risk of toxic or other undesirable effects. In addition,
XX because the amount of protein administered is less, the cost of the unit
XX dosage form to the patient is reduced
XX Sequence 146 AA;
XX Query Match 100.0%; Score 736; DB 2; Length 146;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-73;
XX Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
|||||

Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Qy 61 YQOILTSMPERNVIOISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQOILTSMPERNVIOISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVALSRLQGSLOQDLMLWQLDLSFGC 146
Db 121 TEVALSRLQGSLOQDLMLWQLDLSFGC 146
RESULT 10
AAW34483
ID AAW34483 standard; protein; 146 AA.
XX AC AAW34483;
XX 17-MAR-1998 (first entry)
XX Human obesity protein.
XX Obesity protein; therapy; obesity associated disorder; human.
XX Homo sapiens.
XX EP784981-A2.
XX 23-JUL-1997.
XX 17-JAN-1997; 97EP-00300300.
XX 19-JAN-1996; 96US-0010357P.
XX 07-FEB-1996; 96GB-00002410.
XX (ELIL) LILLY & CO ELI.
XX Beals JM, Dodd SW, Millican RL, Pekar AH;
XX WPI; 1997-365737/34.
XX New obesity protein compositions - comprising a soluble parenteral
XX formulation containing a preservative and having low ionic strength.
XX Disclosure; Page 7; 17pp; English.
XX This sequence represents the human obesity protein. It can be used in the
XX formulation of the invention. The formulation of the invention is a
XX soluble parenteral formulation that comprises an obesity protein and a
XX preservative, the formulation having an ionic strength of less than about
XX 10 mM. The compositions can be used for treating obesity and disorders
XX associated with obesity. In the formulations the obesity protein remains
XX soluble at much higher concentration and at the desired pH range
XX Sequence 146 AA;
XX Query Match 100.0%; Score 736; DB 2; Length 146;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-73;
XX Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Qy 61 YQOILTSMPERNVIOISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQOILTSMPERNVIOISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVALSRLQGSLOQDLMLWQLDLSFGC 146
Db 121 TEVALSRLQGSLOQDLMLWQLDLSFGC 146
RESULT 11

[illegible]

CC and a preservative selected from an alkylparaben, chlorobutanol, or a
 CC mixture. The compositions can be used for the treatment of obesity and
 CC disorders associated with obesity. In the formulations, the obesity
 CC protein analogue remains stable and soluble at much higher concentrations
 CC and at a pH range acceptable for a soluble, multi-use parenteral
 CC formulation

XX Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;

Best Local Similarity 100.0%; Pred. No. 7.8e-73; Indels 0; Gaps 0;

Matches 146; Conservative 0; Mismatches 0;

QY 1 VPIQKQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Db 1 VPIQKQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPNRNVIQISNDLENLRLHLVLAFLSKSCHLPWASGLETLDSLGVLASGYS 120

Db 61 YQOILTSMPNRNVIQISNDLENLRLHLVLAFLSKSCHLPWASGLETLDSLGVLASGYS 120

QY 121 TEWVALSRLOGLQDMLWQDLSPGC 146

Db 121 TEWVALSRLOGLQDMLWQDLSPGC 146

RESULT 13

AAW69682

ID AAW69682 standard; protein; 146 AA.

XX AC AAW69682;

XX DT 07-DEC-1998 (first entry)

XX DE Human obesity protein.

XX KW Obesity protein; therapy; human.

XX OS Homo sapiens.

XX PN WO9831391-A1.

XX PD 23-JUL-1998.

XX PF 16-JAN-1998; 98WO-US000939.

XX PR 17-JAN-1997; 97US-0035714P.

XX PR 07-AUG-1997; 97US-0054886P.

XX PA (ELIL) LILLY & CO ELI.

XX PI Rinella JV;

XX DR WPI; 1998-413818/35.

XX Obesity protein, soluble formulation for treating obesity - has pH greater
 XX than 8.0, at which aggregation of obesity proteins by preservatives is
 XX reduced allowing production of multi-use formulation.

XX PS Disclosure; Page 11-12; 30pp; English.

XX This is the amino acid sequence of human obesity protein. The invention
 CC discloses a storage-stable, soluble formulation comprising an obesity
 CC protein and a preservative, and having a pH greater than 8.0. The obesity
 CC protein used in the formulation is preferably bio-synthesised in a host
 CC cell transformed with a recombinant DNA comprising a synthetic or semi-
 CC synthetic DNA encoding tge protein. The soluble formulation can be
 CC administered to mammals to treat obesity (claimed), especially humans
 CC when the obesity protein is human obesity protein. It was found that the
 CC physical stability of obesity proteins in the presence of preservatives
 CC such as phenol and cresol changes abruptly and is greatly enhanced at pH
 CC values above 8.0, such that the aggregation of obesity proteins caused by
 CC preservatives is reduced. At pH above 8.0, obesity proteins remain in

CC solution in the presence of certain preservatives, making possible a
 CC multi-use parenteral formulation containing those preservatives

XX Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;

Best Local Similarity 100.0%; Pred. No. 7.8e-73;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Db 1 VPIQKQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPNRNVIQISNDLENLRLHLVLAFLSKSCHLPWASGLETLDSLGVLASGYS 120

Db 61 YQOILTSMPNRNVIQISNDLENLRLHLVLAFLSKSCHLPWASGLETLDSLGVLASGYS 120

QY 121 TEWVALSRLOGLQDMLWQDLSPGC 146

Db 121 TEWVALSRLOGLQDMLWQDLSPGC 146

RESULT 14

AAW53342

ID AAW53342 standard; protein; 146 AA.

XX AC AAW53342;

XX DT 20-JUL-1998 (first entry)

XX DE Obesity protein analogue formula II SEQ ID NO:4.

XX KW Human; obesity protein; soluble; parenteral formulation; anionic;

XX KW amphiphilic; ob gene; Ob protein.

XX OS Synthetic.

XX Key Location/Qualifiers

XX FH Misc-difference 97

XX FT /note= "His can be replaced with Gln, Asn, Ala, Gly, Ser,

XX or Pro"

XX FT Misc-difference 100

XX FT /note= "Trp can be replaced with Ala, Glu, Asp, Asn, Met,

XX Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu"

XX FT Misc-difference 101

XX FT /note= "Ala can be replaced with Ser, Asn, Gly, His, Pro,

XX Thr, Val"

XX FT Misc-difference 102

XX FT /note= "Ser can be replaced with Arg"

XX FT Misc-difference 103

XX FT /note= "Gly can be replaced with Ala"

XX FT Misc-difference 105

XX FT /note= "Glu can be replaced with Gln"

XX FT Misc-difference 106

XX FT /note= "Thr can be replaced with Lys or Ser"

XX FT Misc-difference 107

XX FT /note= "Leu can be replaced with Pro"

XX FT Misc-difference 108

XX FT /note= "Asp can be replaced with Glu"

XX FT Misc-difference 111

XX FT /note= "Gly can be replaced with Asp"

XX FT Misc-difference 138

XX FT /note= "Trp can be replaced with Ala, Glu, Asp, Asn, Met,

XX Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu; or a

XX pharmacaceutically acceptable salt thereof"

XX EP827750-A2.

XX 11-MAR-1998.

XX 22-AUG-1997; 97EP-00306420.

XX 23-AUG-1996; 96US-0024121P.

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PR 23-AUG-1996; 96US-0025207P.
PA (ELIL ) LILLY & CO ELI.
XX
XX
PI Beals JM, Rinella JV;
XX
XX WPI, 1998-180894/17.
DR
XX Parenteral obesity protein formulations - containing anionic amphiphilic
PT solubiliser and stabiliser.
XX
XX Disclosure; Page 9; 45pp; English.
XX
CC The present sequence represents an obesity protein generic formula for
CC producing obesity protein analogues for use in the present invention as
CC part of a soluble parenteral formulation. The soluble parenteral
CC formulations comprises an obesity protein or obesity protein analogue and
CC an anionic amphiphilic compound. The formulations are used for treating
CC obesity and associated disorders. The proteins are preferably present at
CC a concentration of 5-50 mg/ml. The anionic amphiphilic compound
CC solubilises and stabilises the protein
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKVTGLDFIPGLHPILTILSKMDQTILAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKVTGLDFIPGLHPILTILSKMDQTILAV 60

QY 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSHLPWASGLETTLSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSHLPWASGLETTLSLGGVLEASGYS 120

QY 121 TEVVALSRLOGLQDMLWQLDLSGCC 146
Db 121 TEVVALSRLOGLQDMLWQLDLSGCC 146

RESULT 15
AAY43311
ID AAY43311 standard; protein; 146 AA.
XX
XX AC
XX
XX 21-JAN-2000 (first entry)
XX
XX Human leptin.
XX
KW Leptin; brain function improver; brain denaturation disease; therapy;
KW Alzheimer's disease; old age dementia; Pick's disease;
KW hereditary aphasia; Huntington's chorea; Parkinson's disease;
KW progressive subcutaneous gliosis; progressive supranuclear paralysis;
KW thalamus denaturation; myoclonus epilepsy.
XX
OS Homo sapiens.
XX
XX JP11279074-A.
XX
XX 12-OCT-1999.
XX
XX 26-MAR-1998; 98JP-00100202.
XX
XX 26-MAR-1998; 98JP-00100202.
XX
XX (OMUR/) OMURA H.
XX (HORI/) HORI N.
XX (SHIR/) SHIRAIISHI T.
XX (SASA/) SASAKI K.
XX (TAKE/) TAKEDA H.
XX (TSUJ/) TSUJI M.

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PA (MATS/) MATSUMIYA T.
XX
XX WPI; 1999-629222/54.
XX
XX A brain function improver - useful for treating brain disorientation
PT diseases.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC This sequence represents human leptin. The invention relates to a brain
CC function improver containing mammalian leptin as the active component.
CC The brain function improver is useful as a treating agent for brain
CC denaturation diseases such as Alzheimer's disease, old age dementia,
CC Pick's disease, Huntington's chorea, Parkinson's disease, Parkinson
CC syndrome, progressive subcutaneous gliosis, progressive supranuclear
CC paralysis, thalamus denaturation, hereditary aphasia and myoclonus
CC epilepsy, and other diseases causing deterioration of brain function
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKVTGLDFIPGLHPILTILSKMDQTILAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKVTGLDFIPGLHPILTILSKMDQTILAV 60

QY 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSHLPWASGLETTLSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSHLPWASGLETTLSLGGVLEASGYS 120

QY 121 TEVVALSRLOGLQDMLWQLDLSGCC 146
Db 121 TEVVALSRLOGLQDMLWQLDLSGCC 146

Search completed: March 12, 2005, 04:59:56
Job time : 118.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:33 ; Search time 28.4537 Seconds
(without alignments)
383.035 Million cell updates/sec

Title: US-10-049-182-6

Perfect score: 736

Sequence: 1 VPIQKVQDDTKTLIKTIVTR.....SRLOSLQDMLWLQDLSFGC 146

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	146	1	US-08-398-021-3
2	736	100.0	146	2	US-08-788-943A-5
3	736	100.0	146	2	US-08-823-104-3
4	736	100.0	146	2	US-09-003-081-6
5	736	100.0	146	3	US-08-648-262-6
6	736	100.0	146	3	US-08-648-263-6
7	736	100.0	146	3	US-08-914-375C-32
8	736	100.0	146	4	US-09-172-644-1
9	736	100.0	146	4	US-09-221-178-1
10	736	100.0	146	4	US-09-200-919-1
11	736	100.0	146	5	PCT-US96-00952-2
12	736	100.0	146	5	PCT-US96-00952-3
13	736	100.0	147	4	US-09-200-919-4
14	736	100.0	148	1	US-08-429-362-3
15	736	100.0	148	2	US-08-823-104-18
16	736	100.0	167	2	US-08-540-242A-4
17	736	100.0	167	2	US-08-347-563A-4
18	736	100.0	167	2	US-09-003-081-5
19	736	100.0	167	3	US-08-292-345B-4
20	736	100.0	167	3	US-08-648-262-5
21	736	100.0	167	3	US-08-648-263-5
22	736	100.0	167	3	US-08-485-942A-4
23	736	100.0	167	3	US-08-488-214A-4
24	736	100.0	167	3	US-08-488-208A-4
25	736	100.0	167	3	US-08-759-628-1
26	736	100.0	167	3	US-08-688-908-7
27	736	100.0	167	3	US-08-483-211A-4

28	736	100.0	167	3	US-08-488-223A-4	Sequence 4, Appli
29	736	100.0	167	3	US-09-147-805-4	Sequence 4, Appli
30	736	100.0	167	4	US-08-438-431A-4	Sequence 4, Appli
31	736	100.0	167	4	US-08-488-225A-4	Sequence 4, Appli
32	736	100.0	167	4	US-09-204-730B-4	Sequence 4, Appli
33	736	100.0	167	4	US-09-316-393-4	Sequence 4, Appli
34	736	100.0	167	4	US-09-377-081-17	Sequence 17, Appli
35	736	100.0	167	4	US-09-686-647A-4	Sequence 4, Appli
36	736	100.0	167	5	PCT-US96-01471-4	Sequence 4, Appli
37	736	100.0	397	4	US-08-775-066-2	Sequence 2, Appli
38	733	99.6	146	3	US-08-914-375C-34	Sequence 34, Appli
39	733	99.3	146	2	US-08-788-943A-2	Sequence 2, Appli
40	731	99.3	146	2	US-08-788-943A-3	Sequence 3, Appli
41	731	99.3	146	2	US-08-823-104-11	Sequence 11, Appli
42	731	99.3	146	2	US-08-823-104-12	Sequence 12, Appli
43	731	99.3	146	3	US-08-674-774-3	Sequence 3, Appli
44	731	99.3	147	3	US-08-485-942A-97	Sequence 97, Appli
45	731	99.3	147	3	US-08-488-214A-97	Sequence 97, Appli

ALIGNMENTS

RESULT 1
US-08-398-021-3
; Sequence 3, Application US/08398021
; Patent No. 5594101
; GENERAL INFORMATION:
; APPLICANT: Becker, Gerald W.
; APPLICANT: Hale, John E., Warren C.
; APPLICANT: Mackellar 1, Warren C.
; TITLE OF INVENTION: ANTI-OBESITY PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,021
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P.
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-0757
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-398-021-3

Query Match 100.0%; Score 736; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSKQVKTGLDFPGLHPIILTSKMDQTLAV 60

Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSKQVKTGLDFPGLHPIILTSKMDQTLAV 60

QY 61 YQOILTSMPNRVQISNDLENLRDLHLVLAFAFSKSLPWAAGLETLDLSLGGVLEASGYS 120
Db 61 YQOILTSMPNRVQISNDLENLRDLHLVLAFAFSKSLPWAAGLETLDLSLGGVLEASGYS 120
QY 121 TEVALSRLOGLQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 2

US-08-788-943A-5
; Sequence 5, Application US/08788943A
; Patent No. 5831017
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, James Arthur
; TITLE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND
; FORMULATIONS THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,943A
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10540
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0757
; TELEFAX: (317) 277-1917
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-788-943A-5

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKLTIKTIYTRINDISHTQSVSQKQVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKLTIKTIYTRINDISHTQSVSQKQVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSMPNRVQISNDLENLRDLHLVLAFAFSKSLPWAAGLETLDLSLGGVLEASGYS 120
Db 61 YQOILTSMPNRVQISNDLENLRDLHLVLAFAFSKSLPWAAGLETLDLSLGGVLEASGYS 120
QY 121 TEVALSRLOGLQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 3

US-08-823-104-3
; Sequence 3, Application US/08823104
; Patent No. 5840517
; GENERAL INFORMATION:
; APPLICANT: Atkinson, Paul R

; APPLICANT: Foster, Lisa K
; APPLICANT: Furman, Thomas C
; APPLICANT: Mackellar, Warren C
; TITLE OF INVENTION: Process for Preparing Obesity Protein
; TITLE OF INVENTION: Analogs
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly & Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,104
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/429,362
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36467
; REFERENCE/DOCKET NUMBER: 10022A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-8110
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 97
; OTHER INFORMATION: /note= "His at position 97 is
; OTHER INFORMATION: replaced with Gln, Asn, Ala, Gly, Ser, or Pro"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 100
; OTHER INFORMATION: /note= "Trp at position 100 is
; OTHER INFORMATION: replaced with Ala, Glu, Asp, Asn, Met, Ser, Thr, or Gly"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 101
; OTHER INFORMATION: /note= "Ala at position 101 is
; OTHER INFORMATION: replaced with Ser, Asn, Gly, His, Pro, Thr, or Val"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 102
; OTHER INFORMATION: /note= "Ser at position 102 is
; OTHER INFORMATION: replaced with Arg"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 103
; OTHER INFORMATION: /note= "Gly at position 103 is
; OTHER INFORMATION: replaced with Ala"

NAME/KEY: Modified-site
LOCATION: 105
OTHER INFORMATION: /note= "Glu at position 105 is
OTHER INFORMATION: replaced with Gln"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 106
OTHER INFORMATION: /note= "Thr at position 106 is
OTHER INFORMATION: replaced with Lys or Ser"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 107
OTHER INFORMATION: /note= "Leu at position 107 is
OTHER INFORMATION: replaced with Pro"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 111
OTHER INFORMATION: /note= "Gly at position 111 is
OTHER INFORMATION: replaced with Asp"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 118
OTHER INFORMATION: /note= "Gly at position 118 is
OTHER INFORMATION: replaced with Leu"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 138
OTHER INFORMATION: /note= "Trp at position 138 is
OTHER INFORMATION: replaced with Ala, Glu, Asp, Asn, Met, Ser, Thr, or Gly"
US-08-823-104-3

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQIILTSPSRNVIQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
DB 61 YQIILTSPSRNVIQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
QY 121 TEVALSRQGLQDMLWOLDLSPGC 146
DB 121 TEVALSRQGLQDMLWOLDLSPGC 146

RESULT 4
US-09-003-081-6
Sequence 6, Application US/09003081
Patent No. 5968779
GENERAL INFORMATION:
APPLICANT: Campfield, Arthur Dr.
APPLICANT: Devos, Rene Dr.
APPLICANT: Guisez, Yves Dr.
TITLE OF INVENTION: Recombinant Obese (OB) Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche, Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,081
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/435,777
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Picut, Catherine A.
REGISTRATION NUMBER: 37419
REFERENCE/DOCKET NUMBER: 9165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4387
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-003-081-6
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQIILTSPSRNVIQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
DB 61 YQIILTSPSRNVIQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
QY 121 TEVALSRQGLQDMLWOLDLSPGC 146
DB 121 TEVALSRQGLQDMLWOLDLSPGC 146

RESULT 5
US-08-648-262-6
Sequence 6, Application US/08648262
Patent No. 6025324
GENERAL INFORMATION:
APPLICANT: Bailon, Pascal Mr.
APPLICANT: Campfield, Arthur Dr.
APPLICANT: Devos, Rene Dr.
APPLICANT: Guisez, Yves Dr.
TITLE OF INVENTION: Pegylated Obese (OB) Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche, Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/648,262
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Epstein, William H.
REGISTRATION NUMBER: 20008
REFERENCE/DOCKET NUMBER: 9281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-3723
TELEFAX: (201) 235-2363

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-648-262-6

Query Match      100.0%; Score 736; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
QY 61 YQQLITSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQQLITSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
QY 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 6
US-08-648-263-6
; Sequence 6, Application US/08648263
; Patent No. 6025325
; GENERAL INFORMATION:
; APPLICANT: Campfield, Arthur
; APPLICANT: Devos, Rene
; TITLE OF INVENTION: RECOMBINANT OBESE (OB) PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/648,263
; FILING DATE: 15-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,629
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,777
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kreisler, Lewis J
; REGISTRATION NUMBER: 38522
; REFERENCE/DOCKET NUMBER: RAN 4105/175-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)235-4387
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
US-08-648-263-6

Query Match      100.0%; Score 736; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
QY 61 YQQLITSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQQLITSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
QY 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 7
US-08-914-375C-32
; Sequence 32, Application US/08914375C
; Patent No. 6377893
; GENERAL INFORMATION:
; APPLICANT: Steven A. Benner
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: 1501 NW 68th Terrace
; CITY: Gainesville
; STATE: FL
; COUNTRY: United States
; ZIP: 32605-4147
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,375C
; FILING DATE: 19-Aug-1997
; CLASSIFICATION: 702/20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352 392 7773
; TELEFAX: 352 331 0462
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: leptin
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-914-375C-32

Query Match      100.0%; Score 736; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
QY 61 YQQLITSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQQLITSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
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Qy 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
|
Db 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 8

US-09-172-644-1
; Sequence 1, Application US/09172644
; Patent No. 6420339
; GENERAL INFORMATION:
; APPLICANT: KINSTLER, OLAF
; TITLE OF INVENTION: SITE-DIRECTED DUAL PEGYLATION OF PROTEINS FOR IMPROVED
; FILE REFERENCE: A-567
; CURRENT APPLICATION NUMBER: US/09/172,644
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-09-172-644-1

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
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Db 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|
Qy 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSLPWSAGLETLSLGGVLEASGYS 120
|
Db 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSLPWSAGLETLSLGGVLEASGYS 120
|
Qy 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
|
Db 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 9

US-09-221-178-1
; Sequence 1, Application US/09221178
; Patent No. 6451346
; GENERAL INFORMATION:
; APPLICANT: SHAH, SUBODH
; APPLICANT: DAI, WEIGUO
; TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR
; FILE REFERENCE: A-575
; CURRENT APPLICATION NUMBER: US/09/221,178
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-09-221-178-1

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|
Db 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|
Qy 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSLPWSAGLETLSLGGVLEASGYS 120
|

Db 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSLPWSAGLETLSLGGVLEASGYS 120
|
Qy 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
|
Db 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 10

US-09-200-919-1
; Sequence 1, Application US/09200919
; Patent No. 6518235
; GENERAL INFORMATION:
; APPLICANT: COMURA, YUTAKA
; APPLICANT: HORI, NOBUAKI
; APPLICANT: SHIRAIISHI, TAKEMASA
; APPLICANT: SASAKI, KAZUO
; APPLICANT: TAKEDA, HIROSHI
; APPLICANT: TSUJIT, MINORU
; APPLICANT: MATSUMIYA, TERUHIKO
; TITLE OF INVENTION: DRUG FOR IMPROVEMENT OF BRAIN FUNCTION
; FILE REFERENCE: YAMA-100
; CURRENT APPLICATION NUMBER: US/09/200,919
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: HUMAN
US-09-200-919-1

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
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Db 1 VPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|
Qy 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSLPWSAGLETLSLGGVLEASGYS 120
|
Db 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSLPWSAGLETLSLGGVLEASGYS 120
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Qy 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
|
Db 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 11

PCT-US96-00952-2
; Sequence 2, Application PC/TUS9600952
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Obesity Proteins
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00952
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-00952-2

Query Match 100.0%; Score 736; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
QY 61 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAFSKSHLPWASGLETLDSLGGVLEASGYS 120
DB 61 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAFSKSHLPWASGLETLDSLGGVLEASGYS 120
QY 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146
DB 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 12

PCT-US96-00952-3
; Sequence 3, Application PC/TUS9600952
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Obesity Proteins
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00952
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-00952-3

Query Match 100.0%; Score 736; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
QY 61 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAFSKSHLPWASGLETLDSLGGVLEASGYS 120
DB 61 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAFSKSHLPWASGLETLDSLGGVLEASGYS 120
QY 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146
DB 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 13

US-09-200-919-4
; Sequence 4, Application US/09200919
; Patent No. 6518235
; GENERAL INFORMATION:
; APPLICANT: OOMURA, YUTAKA
; APPLICANT: HORI, NOBUAKI
; APPLICANT: SHIRAI, TAKEMASA
; APPLICANT: SASAKI, KAZUO
; APPLICANT: TAKEDA, HIROSHI
; APPLICANT: TSUJI, MINORU
; APPLICANT: MATSUMIYA, TERUHIKO
; TITLE OF INVENTION: DRUG FOR IMPROVEMENT OF BRAIN FUNCTION
; FILE REFERENCE: YAMA-100

; CURRENT APPLICATION NUMBER: US/09/200,919
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 147
; TYPE: PRT
; ORGANISM: HUMAN
US-09-200-919-4

Query Match 100.0%; Score 736; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
DB 2 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 61
QY 61 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAFSKSHLPWASGLETLDSLGGVLEASGYS 120
DB 62 YQQLTSMPSRNVIIQISNDLENLRLDLHLVLAFAFSKSHLPWASGLETLDSLGGVLEASGYS 121
QY 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146
DB 122 TEVVALSRLOGSLQDMLWQLDLSGPC 147

RESULT 14

US-08-429-362-3
; Sequence 3, Application US/08429362
; Patent No. 5614379
; GENERAL INFORMATION:
; APPLICANT: Mackellar, Warren C.
; TITLE OF INVENTION: Process For Preparing Anti-Obesity
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/Patent Division
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,362
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P.
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0757
; TELEFAX: (317) 277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-429-362-3

Query Match 100.0%; Score 736; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Db 3 VPIQKVQDDTKILIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLTKMDQTLAV 62
Qy 61 YQOILTSPSRNVIOISNDLENRLDLLHLVLAFAFSKSLPWPASGLETTLDLSLGGVLEASGYS 120
Db 63 YQOILTSPSRNVIOISNDLENRLDLLHLVLAFAFSKSLPWPASGLETTLDLSLGGVLEASGYS 122
Qy 121 TEVVALSRLOQSLQDMLWQLDLSFGC 146
Db 123 TEVVALSRLOQSLQDMLWQLDLSFGC 148

RESULT 15

US-08-823-104-18
; Sequence 18, Application US/08823104
; Patent No. 5840517
; GENERAL INFORMATION:
; APPLICANT: Atkinson, Paul R
; APPLICANT: Foster, Lisa K
; APPLICANT: Furman, Thomas C
; APPLICANT: Mackellar, Warren C
; TITLE OF INVENTION: Process for Preparing Obesity Protein
; TITLE OF INVENTION: Analogs
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly & Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,104
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/429,362
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36467
; REFERENCE/DOCKET NUMBER: 10022A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-8110
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-823-104-18

Query Match 100.0%; Score 736; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKILIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 3 VPIQKVQDDTKILIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLTKMDQTLAV 62
Qy 61 YQOILTSPSRNVIOISNDLENRLDLLHLVLAFAFSKSLPWPASGLETTLDLSLGGVLEASGYS 120
Db 63 YQOILTSPSRNVIOISNDLENRLDLLHLVLAFAFSKSLPWPASGLETTLDLSLGGVLEASGYS 122

Qy 121 TEVVALSRLOQSLQDMLWQLDLSFGC 146
Db 123 TEVVALSRLOQSLQDMLWQLDLSFGC 148

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Job time : 29.4537 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 05:03:46 ; Search time 82.0958 Seconds
(without alignments)
586.599 Million cell updates/sec

Title: US-10-049-182-6
Perfect score: 736
Sequence: 1 VPIQVQDDTKTLIKTIIVTR.....SRLOGLQDMLWQLDLSPEC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA.*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736	100.0	146	US-10-191-377-1	Sequence 1, Appli
2	736	100.0	146	US-10-139-794-10	Sequence 10, Appli
3	736	100.0	146	US-10-419-058-2	Sequence 2, Appli
4	736	100.0	146	US-10-467-114-1	Sequence 1, Appli
5	736	100.0	146	US-10-622-998-1	Sequence 1, Appli
6	736	100.0	146	US-10-658-834A-211	Sequence 211, App
7	736	100.0	146	US-10-468-496-1	Sequence 1, Appli
8	736	100.0	146	US-10-872-198-127	Sequence 127, App
9	736	100.0	146	US-10-623-189-1	Sequence 1, Appli
10	736	100.0	167	US-09-736-084-4	Sequence 4, Appli
11	736	100.0	167	US-09-928-522-7	Sequence 7, Appli
12	736	100.0	167	US-09-789-306-3	Sequence 3, Appli
13	736	100.0	167	US-09-804-409A-11	Sequence 11, Appli

14	736	100.0	167	10	US-09-316-393-4	Sequence 4, Appli
15	736	100.0	167	15	US-10-440-464-67	Sequence 67, Appli
16	736	100.0	167	15	US-10-458-334-17	Sequence 17, Appli
17	736	100.0	167	17	US-10-698-510-17	Sequence 17, Appli
18	736	100.0	374	15	US-10-679-999-15	Sequence 15, Appli
19	736	100.0	374	15	US-10-679-999-18	Sequence 18, Appli
20	736	100.0	379	15	US-10-679-999-9	Sequence 9, Appli
21	736	100.0	379	15	US-10-679-999-12	Sequence 12, Appli
22	736	100.0	396	9	US-09-859-361-2	Sequence 2, Appli
23	736	100.0	396	9	US-09-859-361-5	Sequence 5, Appli
24	736	100.0	397	8	US-08-779-457-47	Sequence 47, Appli
25	736	100.0	397	17	US-10-921-710-47	Sequence 47, Appli
26	736	100.0	399	9	US-09-859-361-7	Sequence 7, Appli
27	736	100.0	401	9	US-09-859-361-9	Sequence 9, Appli
28	734	99.7	146	16	US-10-658-834A-666	Sequence 666, App
29	734	99.7	146	16	US-10-658-834A-672	Sequence 672, App
30	734	99.7	146	16	US-10-658-834A-677	Sequence 677, App
31	734	99.7	146	16	US-10-658-834A-683	Sequence 683, App
32	733	99.6	146	16	US-10-658-834A-665	Sequence 665, App
33	733	99.6	146	16	US-10-658-834A-671	Sequence 671, App
34	733	99.6	146	16	US-10-658-834A-673	Sequence 673, App
35	733	99.6	146	16	US-10-658-834A-676	Sequence 676, App
36	733	99.6	146	16	US-10-658-834A-682	Sequence 682, App
37	731	99.3	146	9	US-09-850-433-4	Sequence 4, Appli
38	731	99.3	146	16	US-10-658-834A-674	Sequence 674, App
39	731	99.3	146	16	US-10-658-834A-675	Sequence 675, App
40	731	99.3	146	16	US-10-658-834A-679	Sequence 679, App
41	731	99.3	146	16	US-10-658-834A-681	Sequence 681, App
42	731	99.3	147	9	US-09-366-133-6	Sequence 6, Appli
43	731	99.3	147	9	US-09-736-084-97	Sequence 97, Appli
44	731	99.3	147	9	US-09-859-768-4	Sequence 4, Appli
45	731	99.3	147	10	US-09-094-931-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-191-377-1
; Sequence 1, Application US/10191377
; Publication No. US20030099709A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR
; TITLE OF INVENTION: SUSTAINED DELIVERY OF BIOLOGICALLY ACTIVE AGENTS
; FILE REFERENCE: A-575
; CURRENT APPLICATION NUMBER: US/10/191,377
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-10-191-377-1

Query Match 100.0%; Score 736; DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VPIQVQDDTKTLIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLKMDQTLAV	60
Db	1	VPIQVQDDTKTLIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLKMDQTLAV	60
Qy	61	YQOILTSMPNRNVIQISNDLENRLDLHLVLAFLAFKSCHPWASGLTDLGGLVLEASGYS	120
Db	61	YQOILTSMPNRNVIQISNDLENRLDLHLVLAFLAFKSCHPWASGLTDLGGLVLEASGYS	120
Qy	121	TEVALSRLOGLQDMLWQLDLSPEC	146
Db	121	TEVALSRLOGLQDMLWQLDLSPEC	146

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RESULT 2
US-10-139-794-10
; Sequence 10, Application US/10139794
; Publication No. US20030232421A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS, LYNX THERAPEUTICS INC.
; APPLICANT: Pierre Legrain, Simon Whiteside, Jen-I Mao, Irina Khrebtukova, Shujun Luo
; TITLE OF INVENTION: Protein-Protein Interactions In Adipocyte Cells (3)
; FILE REFERENCE: B4883A
; CURRENT APPLICATION NUMBER: US/10/139,794
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/288,885
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 2930
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Translation of SEQ ID NO:9
US-10-139-794-10

Query Match      100.0%; Score 736; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSKCHLPWASGLETLDSLGGVLEASGYS 120
Db      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSKCHLPWASGLETLDSLGGVLEASGYS 120

Qy      121 TEVALSRLOGLQDMLWQLDLSGPC 146
Db      121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 3
US-10-419-058-2
; Sequence 2, Application US/10419058
; Publication No. US20040053366A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Zhang, Jinyang
; APPLICANT: Gillies, Stephen D.
; TITLE OF INVENTION: Expression and Export of Anti-Obesity Proteins as Fc
; FILE REFERENCE: LEX-008
; CURRENT APPLICATION NUMBER: US/10/419,058
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US/09/479,508
; PRIOR FILING DATE: 2000-01-07
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-419-058-2

Query Match      100.0%; Score 736; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db      1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSKCHLPWASGLETLDSLGGVLEASGYS 120
Db      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSKCHLPWASGLETLDSLGGVLEASGYS 120

Qy      121 TEVALSRLOGLQDMLWQLDLSGPC 146
Db      121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 5
US-10-622-998-1
; Sequence 1, Application US/10622998
; Publication No. US20040105840A1
; GENERAL INFORMATION:
; APPLICANT: Kinastler, Olaf
; APPLICANT: Ladd, David
; APPLICANT: Papisov, Mikhail
; TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOCOMPATIBLE, BIODEGRADABLE
; FILE REFERENCE: A-822
; CURRENT APPLICATION NUMBER: US/10/622,998
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/397,509
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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Qy      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSKCHLPWASGLETLDSLGGVLEASGYS 120
Db      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSKCHLPWASGLETLDSLGGVLEASGYS 120

Qy      121 TEVALSRLOGLQDMLWQLDLSGPC 146
Db      121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 4
US-10-467-114-1
; Sequence 1, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-115
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-467-114-1

Query Match      100.0%; Score 736; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db      1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSKCHLPWASGLETLDSLGGVLEASGYS 120
Db      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSKCHLPWASGLETLDSLGGVLEASGYS 120

Qy      121 TEVALSRLOGLQDMLWQLDLSGPC 146
Db      121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 5
US-10-622-998-1
; Sequence 1, Application US/10622998
; Publication No. US20040105840A1
; GENERAL INFORMATION:
; APPLICANT: Kinastler, Olaf
; APPLICANT: Ladd, David
; APPLICANT: Papisov, Mikhail
; TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOCOMPATIBLE, BIODEGRADABLE
; FILE REFERENCE: A-822
; CURRENT APPLICATION NUMBER: US/10/622,998
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/397,509
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-622-998-1

Query Match      100.0%; Score 736; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCCHLPWASGLETLDLSLGGVLEASGYS 120
DB 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCCHLPWASGLETLDLSLGGVLEASGYS 120
QY 121 TEVVALSRLOQSLQDMLWQDLSPGC 146
DB 121 TEVVALSRLOQSLQDMLWQDLSPGC 146

RESULT 6
US-10-658-834A-211
; Sequence 211, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dritanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; FILE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: Genbank AAA60470
; DATABASE ENTRY DATE: 1995-01-13
US-10-658-834A-211

Query Match      100.0%; Score 736; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCCHLPWASGLETLDLSLGGVLEASGYS 120
DB 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCCHLPWASGLETLDLSLGGVLEASGYS 120
QY 121 TEVVALSRLOQSLQDMLWQDLSPGC 146
DB 121 TEVVALSRLOQSLQDMLWQDLSPGC 146

RESULT 7
US-10-468-496-1
; Sequence 1, Application US/10468496
; Publication No. US20040180386A1

; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-468-496-1

Query Match      100.0%; Score 736; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCCHLPWASGLETLDLSLGGVLEASGYS 120
DB 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCCHLPWASGLETLDLSLGGVLEASGYS 120
QY 121 TEVVALSRLOQSLQDMLWQDLSPGC 146
DB 121 TEVVALSRLOQSLQDMLWQDLSPGC 146

RESULT 8
US-10-872-198-127
; Sequence 127, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KULTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMERIER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
```

; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-127

Query Match 100.0%; Score 736; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60

QY 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALSRQGSLOQDMWLQDLSPGC 146
DB 121 TEVVALSRQGSLOQDMWLQDLSPGC 146

RESULT 9

US-10-623-189-1
; Sequence 1, Application US/10623189
; Publication No. US20050020496A1
; GENERAL INFORMATION:
; APPLICANT: DEPAOLI, Alex M.
; APPLICANT: ORAL, Elif Arioglu
; APPLICANT: TAYLOR, Simeon I.
; APPLICANT: GARG, Abhinav
; TITLE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETERM
; FILE REFERENCE: 54113.8005.US02
; CURRENT APPLICATION NUMBER: US/10/623,189
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/279,129
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 60/336,394
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Leptin Human 146 (rHu-Leptin 1-146)
US-10-623-189-1

Query Match 100.0%; Score 736; DB 17; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60

QY 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALSRQGSLOQDMWLQDLSPGC 146
DB 121 TEVVALSRQGSLOQDMWLQDLSPGC 146

RESULT 10

US-09-328-522-7

; Sequence 7, Application US/09928522

; Patent No. US20020110857A1

; GENERAL INFORMATION:

; APPLICANT: Spurlock, Michael E.

US-09-736-084-4

; Sequence 4, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:

; APPLICANT: THE ROCKEFELLER UNIVERSITY

; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

; NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/736,084

; FILING DATE: 13-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/438,431

; FILING DATE: May 10, 1995

; APPLICATION NUMBER: 08/347,563

; FILING DATE: No. US20020107211A1, November 30, 1994

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 167 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; DESCRIPTION: Human ob polypeptide

; ORIGINAL SOURCE:

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-736-084-4

Query Match 100.0%; Score 736; DB 9; Length 167;

Best Local Similarity 100.0%; Pred. No. 3.8e-72;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60

DB 22 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 81

QY 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

DB 82 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141

QY 121 TEVVALSRQGSLOQDMWLQDLSPGC 146

DB 142 TEVVALSRQGSLOQDMWLQDLSPGC 167

RESULT 11

US-09-328-522-7

; Sequence 7, Application US/09928522

; Patent No. US20020110857A1

; GENERAL INFORMATION:

; APPLICANT: Spurlock, Michael E.

;; TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID
;; SEQUENCES CODING THEREFOR AND USES THEREOF
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.
;; STREET: Suite 2100 111 East Wisconsin Avenue
;; CITY: Milwaukee
;; STATE: Wisconsin
;; COUNTRY: USA
;; ZIP: 53202
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/928,522
;; FILING DATE: 13-Aug-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/688,908
;; FILING DATE: 31-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Plotecher, Gary R.
;; REGISTRATION NUMBER: 27,830
;; REFERENCE/DOCKET NUMBER: PM-8808
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 414-273-2100
;; TELEFAX: 414-223-5000
;; INFORMATION FOR SEQ ID NO: 7:
;;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 167 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;;
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-928-522-7
Query Match 100.0%; Score 736; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;
QY 1 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 22 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
Db 82 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 141
QY 121 TEVVALSRLOQSLQDMLWQLDLSPGC 146
Db 142 TEVVALSRLOQSLQDMLWQLDLSPGC 167
RESULT 12
US-09-789-306-3
; Sequence 3, Application US/09789306
; Patent No. US20020142456A1
; GENERAL INFORMATION:
; APPLICANT: Herndav, Natasha
; TITLE OF INVENTION: Canine OB Protein Compositions and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91320
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/789,306
;; FILING DATE: 20-Feb-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/609,408
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Eggert, Joan D.
;; REFERENCE/DOCKET NUMBER: A-387
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 167 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Leader Sequence
;; LOCATION: -21 to -1
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-789-306-3
Query Match 100.0%; Score 736; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;
QY 1 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 22 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
Db 82 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 141
QY 121 TEVVALSRLOQSLQDMLWQLDLSPGC 146
Db 142 TEVVALSRLOQSLQDMLWQLDLSPGC 167
RESULT 13
US-09-804-409A-11
; Sequence 11, Application US/09804409A
; Patent No. US2002015100A1
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, TIMOTHY J.
; APPLICANT: CHEUNG, ANTHONY T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
; TITLE OF INVENTION: EXPRESSION IN GUT
; FILE REFERENCE: 029996/027 8721
; CURRENT APPLICATION NUMBER: US/09/804,409A
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-804-409A-11
Query Match 100.0%; Score 736; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;
QY 1 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 22 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120

Db 82 YQQLTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 141
Qy 121 TEVVALSRQSGLODMLWQLDLSFGC 146
Db 142 TEVVALSRQSGLODMLWQLDLSFGC 167

RESULT 14
US-09-316-393-4
; Sequence 4, Application US/09316393
; Publication No. US20030040039A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; FILE REFERENCE: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/316,393
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human Ob protein
; ORIGINAL SOURCE: Human
US-09-316-393-4

Query Match 100.0%; Score 736; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSCKQVTKGLDFIPGLHPITLTLKMDQTLAV 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSCKQVTKGLDFIPGLHPITLTLKMDQTLAV 81

Qy 61 YQQLTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Db 82 YQQLTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 141

Qy 121 TEVVALSRQSGLODMLWQLDLSFGC 146
Db 142 TEVVALSRQSGLODMLWQLDLSFGC 167

RESULT 15
US-10-440-464-67

; Sequence 67, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: AND ACTIVITY IN MAMMALS
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-67

Query Match 100.0%; Score 736; DB 15; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSCKQVTKGLDFIPGLHPITLTLKMDQTLAV 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSCKQVTKGLDFIPGLHPITLTLKMDQTLAV 81

Qy 61 YQQLTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Db 82 YQQLTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 141

Qy 121 TEVVALSRQSGLODMLWQLDLSFGC 146
Db 142 TEVVALSRQSGLODMLWQLDLSFGC 167

Search completed: March 12, 2005, 05:21:04
Job time : 83.0958 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:02 ; Search time 22.8562 Seconds
(without alignments)
614.609 Million cell updates/sec

Title: US-10-049-182-6
Perfect score: 736
Sequence: 1 VPIQKVDPTKTLIKTIVTR.....SRLQSLQDMLWQLDLSPGC 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736	100.0	167	1 LTHU	leptin precursor -
2	720.5	97.9	166	2 I53166	leptin precursor -
3	619	84.1	167	1 LTNS	leptin precursor -
4	605	82.2	167	1 LTRT	leptin precursor -
5	605	82.2	167	2 I55622	rat ob - rat
6	81.5	11.1	1600	2 AB3281	glutamate dehydrog
7	80.5	10.9	444	2 S54039	hypothetical prote
8	79	10.7	829	2 T01362	probable myosin he
9	78	10.7	952	2 H84583	hypothetical prote
10	78	10.6	450	2 S75514	sensory transducti
11	78	10.6	639	2 AI0055	probable soluble l
12	77.5	10.5	574	1 B42374	phosphotransferase
13	76.5	10.4	173	2 S77486	ribosomal protein
14	76.5	10.4	362	2 A83967	carbamoyl-phosphat
15	76.5	10.4	822	2 E86305	probable trehalase
16	76	10.3	409	2 B89954	hypothetical prote
17	76	10.3	570	2 T46011	hypothetical prote
18	76	10.3	1036	2 D70117	acriflavine resist
19	75.5	10.3	403	2 T26551	hypothetical prote
20	75.5	10.3	1438	2 S59792	probable membrane
21	75	10.2	142	2 C72430	hypothetical prote
22	75	10.2	296	2 D70424	hypothetical prote
23	75	10.2	424	2 E81358	glutamate-1-semial
24	75	10.2	1191	2 S76414	beta transducin-li
25	74.5	10.1	559	2 AB2202	hypothetical prote
26	74.5	10.1	674	2 S46092	probable membrane
27	74	10.1	177	2 A28106	prolactin, 20K - M
28	74	10.1	200	2 B32477	prolactin II precu
29	74	10.1	421	2 AB2959	exopolysaccharide

30	74	10.1	423	2 D98324	exopolysaccharide
31	74	10.1	462	2 C69676	alkaline phosphata
32	74	10.1	1695	2 A56921	kinesin family pro
33	73.5	10.0	845	2 H71317	probable methyl-ac
34	73.5	10.0	1228	2 S46754	hypothetical prote
35	73	9.9	186	2 G82638	conserved hypochet
36	73	9.9	296	2 D88511	ATP-dependent RNA
37	73	9.9	672	2 D81746	type III secretion
38	73	9.9	696	2 S4912	hypothetical prote
39	73	9.9	790	2 H71509	phenylalanine-TRNA
40	73	9.9	921	2 F71486	probable yopC/gen
41	73	9.9	1119	2 AC0045	probable membrane
42	72.5	9.9	406	2 T47924	hypothetical prote
43	72.5	9.9	424	2 S37780	keratin 20, type I
44	72.5	9.9	462	2 JC5625	14-nm filament pro
45	72.5	9.9	550	2 B84900	hypothetical prote

ALIGNMENTS

RESULT 1

LTHU
leptin precursor - human
N;Alternate names: obese protein; obesity factor
C;Species: Homo sapiens (man)
C;Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: A38952; J00148
R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A;Title: Positional cloning of the mouse obese gene and its human homologue.
A;Reference number: S50863; MUID:95075453; PMID:7984236
A;Accession: A38952
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-167 <ZHA>
A;Cross-references: UNIPROT:P41159; GB:U18915; NID:G623331; PIDN:AAA60470.1; PID:G62333
R;Liao, H.J.; Deng, Y.B.; Chen, X.M.; Ye, Y.Z.
Chinese Biochem. J. 13, 249-253, 1997
A;Title: Cloning of chinese obesity gene and construction of prokaryotic expression vec
A;Reference number: J00148
A;Accession: J00148
A;Molecule type: mRNA
A;Residues: 'M',22-167 <LTA>
A;Experimental source: adipose
A;Note: the author translated GAC for residue 148 as Ser
C;Genetics:
A;Gene: GDB:LEP; OB; OBS
A;Cross-references: GDB:136420; OMIM:164160
A;Map position: 7q31.3-7q31.3
C;Superfamily: leptin
C;Keywords: adipose tissue
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-167/Product: leptin #status predicted <MAT>

Query Match 100.0%; Score 736; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VPIQKVDPTKTLIKTIVTRINDISHTQSVSSKQKVTGLDIFGLHPILTLSKMDQTLAV	60
DB	22	VPIQKVDPTKTLIKTIVTRINDISHTQSVSSKQKVTGLDIFGLHPILTLSKMDQTLAV	81
QY	61	YQOILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS	120
DB	82	YQOILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS	141
QY	121	TEVVALSRQGSLODMLWQLDLSPGC	146
DB	142	TEVVALSRQGSLODMLWQLDLSPGC	167

RESULT 2

```
153166
leptin precursor - human
N:Alternate names: obese
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: I53166; G02328
R:Masuzaki, H.; Ogawa, Y.; Isse, N.; Satoh, N.; Okazaki, T.; Shigemoto, M.; Mori, K.; Tanabe, T.;
Diabetes 44, 855-858, 1995
A:Title: Human obese gene expression. Adipocyte-specific expression and regional difference
A:Reference number: I53166; MUID:95309556; PMID:7789654
A:Accession: I53166
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-166 <RES>
A:Cross-references: UNIPROT:P41159; GB:D49487; NID:G904211; PIDN:BAA08448.1; PID:G904212
R:Chehab, F.F.; Lim, M.E.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01063
A:Accession: G02328
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-166 <CHE>
A:Cross-references: EMBL:U43415; NID:g1163105; PIDN:AAC31660.1; PID:g1163106
C:Genetics:
A:Gene: GDB:IDP; OB; OBS
A:Cross-references: GDB:136420; OMIM:164160
A:Map position: 7q32.1-7q32.1
A:Introns: 48/3
C:Superfamily: leptin

Query Match 97.9%; Score 720.5; DB 2; Length 166;
Best Local Similarity 99.3%; Pred. No. 4.6e-58;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 80

QY 61 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 120
DB 81 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 140

QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 141 TEVVALSRLOGLQDMLWQLDLSGPC 166

RESULT 3
LIMS
leptin precursor - mouse
N:Alternate names: obese protein
C:Species: Mus musculus (house mouse)
C:Date: 14-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: S50863
R:Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A:Title: Positional cloning of the mouse obese gene and its human homologue.
A:Reference number: S50863; MUID:95075453; PMID:7984236
A:Accession: S50863
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-167 <ZHA>
A:Cross-references: UNIPROT:P41160; EMBL:U18812; NID:g746416; PIDN:AAA64564.1; PID:g6032
C:Superfamily: leptin
C:Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 84.1%; Score 619; DB 1; Length 167;
Best Local Similarity 84.9%; Pred. No. 7.1e-49;
Matches 124; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
```

```
DB 22 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSAKQRTGLDFIPGLHPILTLSKMDQTLAV 81

QY 61 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 120
DB 82 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 141

QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 142 TEVVALSRLOGLQDMLWQLDLSGPC 167

RESULT 4
LIMS
leptin precursor - rat
N:Alternate names: obese protein; obesity factor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: PC4034; JC4142
R:Funahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Nozaki, M.
Biochem. Biophys. Res. Commun. 211, 469-475, 1995
A:Title: Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial
A:Reference number: PC4034; MUID:95314614; PMID:7794258
A:Accession: PC4034
A:Molecule type: mRNA
A:Residues: 1-167 <FUN>
A:Cross-references: UNIPROT:P50596
A:Experimental source: adipose tissue
A:Note: The authors translated the codon AAA for residue 32 as Thr
R:Murakami, T.; Shima, K.
Biochem. Biophys. Res. Commun. 209, 944-952, 1995
A:Title: Cloning of rat obese cDNA and its expression in obese rats.
A:Reference number: JC4142; MUID:95251725; PMID:7733988
A:Accession: JC4142
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-167 <MUR>
A:Cross-references: DDBJ:D49653; NID:G995614; PIDN:BAA08529.1; PID:G995615
A:Experimental source: liver
A:Comment: This protein is proposed to function as part of a signalling pathway from ad
C:Genetics:
A:Gene: obese
C:Superfamily: leptin
C:Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 82.2%; Score 605; DB 1; Length 167;
Best Local Similarity 83.6%; Pred. No. 1.3e-47;
Matches 122; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSAKQRTGLDFIPGLHPILTLSKMDQTLAV 81

QY 61 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 120
DB 82 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 141

QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 142 TEVVALSRLOGLQDMLWQLDLSGPC 167

RESULT 5
LIMS
leptin precursor - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I55622
R:Ogawa, Y.; Masuzaki, H.; Isse, N.; Okazaki, T.; Mori, K.; Shigemoto, M.; Satoh, N.; Tanabe, T.
J. Clin. Invest. 96, 1647-1652, 1995
A:Title: Molecular cloning of rat obese cDNA and augmented gene expression in genetically
```

A:Reference number: I55622; MUID:95386724; PMID:7657834
A:Accession: I55622
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-167 <RES>
A:Cross-references: GB:D45862; NID:g1018990; PIDN:BAA08296.1; PID:g1018991
C:Superfamily: lepton

Query Match 82.2%; Score 605; DB 2; Length 167;
Best Local Similarity 83.6%; Pred. No. 1.3e-47;
Matches 122; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 VPIQKQDDTKLTIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 22 VPIHKQDDTKLTIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 61 YQQLTSMPSNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLETLDSLGGLVLEASGY 120
DB 82 YQQLTSLPSQNVQLQIAHLENLRLDHLVAFSKSCHLPQTRGLQRPESLDGVLASLYS 141

QY 121 TEVVALSRLOGLQDMLWQIDLSGPC 146
DB 142 TEVVALSRLOGLQDMLWQIDLSGPC 167

RESULT 6
AB3281
glutamate dehydrogenase (EC 1.4.1.2) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AB3281
R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
.; Mazur, M.; Goldsman, E.; Seikov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3281
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1600 <KUR>
A:Cross-references: UNIPROT:Q8YJ55; GB:AE008917; PIDN:AAL51413.1; PID:g17982118; GSPDB:G
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0231
A:Map position: 1
C:Keywords: oxidoreductase

Query Match 11.1%; Score 81.5; DB 2; Length 1600;
Best Local Similarity 24.6%; Pred. No. 55;
Matches 32; Conservative 23; Mismatches 52; Indels 23; Gaps 5;

QY 6 VDDTKTLTIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVYQQL 65
DB 97 VNDNMPFLDLSINGELND--HTSQI-----FMVHPVLDIRKDELVLIGEAS 143

QY 66 TSPNSNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYTEVVA 125
DB 144 QLAPAKGVERVS-----LVQIHLPAKQAKADLTAGLKR--LGQV--RSAVSDWKPM 193

QY 126 LSRLOGLQD 135
DB 194 LKRLDGAIDD 203

RESULT 7
S54039
hypothetical protein YDR055w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D4214; hypothetical protein YBRB444; hypothetical
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54039; S58835; S61744; S67871
R:Hunt, S.; Bowman, S.; Harris, D.
submitted to the EMBL Data Library, May 1995

A:Reference number: S54031
A:Accession: S54039
A:Molecule type: DNA
A:Residues: 1-444 <HUN>
A:Cross-references: UNIPROT:Q12355; EMBL:Z49209; NID:g798897; PIDN:CAA89084.1; PID:g798
R:Brandt, P.; Otto, B.; Ramlow, S.; Blocker, H.
submitted to the EMBL Data Library, January 1995
A:Reference number: S58832
A:Accession: S58835
A:Molecule type: DNA
A:Residues: 1-444 <BRA>
A:Cross-references: EMBL:X84162; NID:g706817; PIDN:CAA58971.1; PID:g706821
R:Brandt, P.; Ramlow, S.; Otto, B.; Blocker, H.
Yeast 12, 85-90, 1996
A:Title: Nucleotide sequence analysis of a 32,500 bp region of the right arm of Sacchar
A:Reference number: S61741; MUID:96381250; PMID:8789263
A:Accession: S61744
A:Molecule type: DNA
A>Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-444 <BRW>
A:Cross-references: EMBL:X84162; NID:g706817; PIDN:CAA58971.1; PID:g706821
R:Blocker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67587
A:Accession: S67871
A:Molecule type: DNA
A:Residues: 1-444 <BLO>
A:Cross-references: EMBL:Z74351; NID:g1431498; PIDN:CAA98873.1; PID:g1431499; MIPS:YDRO
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PST1
A:Cross-references: SGD:S0002462
A:Map position: 4R
C:Keywords: transmembrane protein
F;5-21/Domain: transmembrane #status predicted <TMM>

Query Match 10.9%; Score 80.5; DB 2; Length 444;
Best Local Similarity 24.3%; Pred. No. 13;
Matches 35; Conservative 23; Mismatches 49; Indels 37; Gaps 6;

QY 2 PIQKQDDTKLTIKIVTRI-----NDIS-----HTQSVSSKQKVTGLDFIPGLHPI 48
DB 181 PVETVSDLSQFSGFNQTKITFDLWANNISUTDVHVSFANLQKINSLSGFINNIS 240

QY 49 LTLKMD---QTLAVYQQLTSMPSNRNVIQISND-----LENLRLDHLVAFSKSCHLP 99
DB 241 LNFTKLNTIGQTFSI-----VSDYLKNSLSTIGGALVVAANTGLQ 285

QY 100 WASGLETLDSLGGLVLEASGYSTEV 123
DB 286 KIGGLDNLTTIGTGLEVVGNFTSL 309

RESULT 8
T01362
probable myosin heavy chain At2g34730 - Arabidopsis thaliana
N:Alternate names: hypothetical protein T29F13.6
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01362; C84760
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
A:Reference number: Z14179
A:Accession: T01362
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-829 <ROU>
A:Cross-references: UNIPROT:O64584; EMBL:AC003096; NID:g3132469; PID:g3132472
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

phosphotransferase system enzyme I (EC 2.7.3.9) - *Staphylococcus carnosus*
C:Species: *Staphylococcus carnosus*
C>Date: 10-Jul-1992 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C:Accession: B42374; S17075
R:Kohlbrecher, D.; Eisermann, R.; Hengstenberg, W.
J. Bacteriol. 174, 2208-2214, 1992
A:Title: *Staphylococcus* phosphoenolpyruvate-dependent phosphotransferase system: molecular studies of the gene product.
A:Reference number: A42374; MUID:92202148; PMID:1551842
A:Accession: B42374
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-574 <KOH>
A:Cross-references: UNIPROT:P23533; GB:M69050; NID:g153073; PIDN:AAA26664.1; PID:g153075
R:Eisermann, R.; Fischer, R.; Kessler, U.; Neubauer, A.; Hengstenberg, W.
Eur. J. Biochem. 197, 9-14, 1991
A:Title: *Staphylococcus* phosphoenolpyruvate-dependent phosphotransferase system. Purification and cloning of the *ptsH* gene.
A:Reference number: S1367; MUID:91200066; PMID:1901791
A:Accession: S17075
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <EIS>
A:Cross-references: EMBL:X60766; NID:g46907; PIDN:CAA43176.1; PID:g46909
C:Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I homologous
C:Keywords: phosphoprotein; phosphotransferase; sugar transport system
F:5-563/Domain: phosphotransferase system enzyme I homology <PTI>

Query Match 10.5%; Score 77.5; DB 1; Length 574;
Best Local Similarity 25.0%; Pred. No. 34;
Matches 32; Conservative 27; Mismatches 54; Indels 15; Gaps 5;

QY 11 KTLIKTIVTR---INDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVYQQILTS 67
Db 188 RTSHSALMSRSLPAWVGTKSTEEVAGDTIVDGMTGDLNPSDEVIAEQE--- 243

QY 68 MFSRNVQIISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGCVLE---ASG---YSTE 122
Db 244 -KRENFQKQELQKLDAESVTA--DGHVLEAANIGTNDLPGVINGAEGIGLYRTE 300

QY 123 VVALSRLO 130
Db 301 FLYMGRDQ 308

RESULT 13
S77486
ribosomal protein S5 - *Synechocystis* sp. (strain PCC 6803)
N/Alternate names: protein sll1812
C:Species: *Synechocystis* sp.
A/Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S77486
R:KaneKO, T.; Sato, S.; Kikani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S77486
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173 <KAN>
A:Cross-references: UNIPROT:P73304; EMBL:D90905; GB:AB001339; NID:g1652360; PIDN:BAA1733
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: rps5
C:Superfamily: ribosomal protein S5/S2
C:Keywords: protein biosynthesis; ribosome

Query Match 10.4%; Score 76.5; DB 2; Length 173;
Best Local Similarity 31.2%; Pred. No. 9.2;
Matches 29; Conservative 12; Mismatches 41; Indels 11; Gaps 3;

QY 6 VDDTKTLIKTIVTRINDISH-TQSVSSKQKVTGLDFIPG-----LHPILTSLKMDQ 56
Db 70 VADGKKQLIEVLTKEKNSITHITNGVSGGAKVVRPAEFGTGTGIAGAVRTVLELAGVK 129

QY 57 TLAVVQQILTSMPSRNVQIISNDLENRLDLHV 89
Db 130 ILA--KQLGSNNPLNNARAANALETILRTFSEV 160

RESULT 14

A83967

carbamoyl-phosphate synthetase (glutaminase subunit) pyrAA [imported] - *Bacillus halodurans*
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: A83967
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and sequencing of the *ptsH* gene.
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: A83967
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <STO>
A:Cross-references: UNIPROT:Q9K9V8; GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BA006
A:Experimental source: strain C-125
C:Genetics:
A:Gene: pyrAA
C:Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbar

Query Match 10.4%; Score 76.5; DB 2; Length 362;
Best Local Similarity 31.0%; Pred. No. 24;
Matches 22; Conservative 15; Mismatches 27; Indels 7; Gaps 3;

QY 78 NDLENRLDLHLVAFSKSCHLP--WASGLETLDSLGCVLEASGYS---TEVVALSRLO 131

Db 66 DDFESNNPAHGLIVKEACDIPSNWSE-ESLDSLKAKQIPGLSGDITFKLTFLRMHG 124

QY 132 SLQDMLWQLDL 142

Db 125 TLKGQLCPLDV 135

RESULT 15

E86305

probable trehalose-6-phosphate synthase [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86305
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86305
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-822 <STO>
A:Cross-references: UNIPROT:Q9FZ57; GB:AE005172; NID:g9802765; PIDN:AAF99834.1; GSPDB:G

A:Map position: 1

Query Match 10.4%; Score 76.5; DB 2; Length 822;
Best Local Similarity 31.6%; Pred. No. 67;
Matches 31; Conservative 16; Mismatches 36; Indels 15; Gaps 4;

QY 38 GLDFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVQIISNDLENRLDLHLVAFSKSCH 97

Db 470 GLDFMSELNGIIPESQM-----RKLPLQPEQDVIIQQYSQNN--RLIILGFFGTIA 521
Qy 98 LPWASGLETLID-----SLGGVLEA--SGYSTEVVALSR 128
Db 522 EPMNSGKEMDLKLNPELXGTLKALCNDPKTTVVVLSR 559

Search completed: March 12, 2005, 05:04:36
Job time : 23.8562 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:44:37 ; Search time 105.419 Seconds
(without alignments)
709.207 Million cell updates/sec

Title: US-10-049-182-6
Perfect score: 736
Sequence: 1 VPIQKVDTKLTIKTIIVR.....SRLOGSLQDMLWQLDLSPQC 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736	100.0	167	1 OB_HUMAN	P41159 homo sapien
2	736	100.0	167	2 Q6NT58	Q6NT58 homo sapien
3	733	99.6	146	1 OB_PANTR	O02750 pan troglod
4	728	98.9	146	1 OB_GORGO	Q95189 gorilla gor
5	721	98.0	146	1 OB_PONPY	Q95234 ponga pygma
6	721	98.0	146	1 OB_PONPY	Q28504 macaca mula
7	639	86.8	167	1 OB_FELCA	Q9N2C1 felis silve
8	628	85.3	146	2 Q6T8R8	Q6T8R8 bubalus bub
9	628	85.3	167	1 OB_BOVIN	P50595 bos taurus
10	627	85.2	167	1 OB_PIG	Q29406 sus scrofa
11	624	84.8	146	1 OB_SHEEP	Q28603 ovis aries
12	619	84.1	167	1 OB_MOUSE	P41160 mus musculus
13	605	82.2	167	1 OB_RAT	P50596 rattus norv
14	586.5	79.7	163	1 OB_CANFA	O02720 canis famil
15	576.5	78.3	145	1 OB_CHICK	O42164 gallus gall
16	576.5	78.3	145	1 OB_MELGA	Q93416 meleagris g
17	522.5	71.0	145	2 Q6S9B2	Q6S9B2 equus cabal
18	505	68.6	167	1 OB_SMICR	Q9XSW9 sminthopsis
19	498	67.7	119	2 Q861R2	Q861R2 bubalus bub
20	477	64.8	118	2 Q8MK60	Q8MK60 alopec lago
21	476	64.7	118	2 Q8MK58	Q8MK58 vulpes vulp
22	474	64.4	118	2 Q8MK59	Q8MK59 nyctereutes
23	469	63.7	118	2 Q8MK61	Q8MK61 canis famil
24	465	63.2	167	2 Q706D0	Q706D0 halichoerus
25	463	62.9	167	2 Q706D1	Q706D1 phoca vitul
26	462	62.8	123	2 Q955W9	Q955W9 myotis luci
27	449	61.0	109	2 Q866S7	Q866S7 bubalus bub
28	447	60.7	99	1 OB_HORSE	Q9TU09 equus cabal
29	439	59.6	109	2 Q864V1	Q864V1 camelus dro
30	387	52.6	106	2 Q95MG5	Q95MG5 capra hircu
31	380	51.6	90	2 Q8WMK7	Q8WMK7 delphinapte

32	376	51.1	90	2 Q7TMN2	Q7tmn2 marmota mon
33	375	51.0	90	2 Q7TMN0	Q7tmn0 tamiasciuru
34	371	50.4	91	2 Q7YR78	Q7yr78 bubalus bub
35	368	50.0	90	2 Q8WML2	Q8wml2 oryctolagus
36	367	49.9	90	2 Q8WML1	Q8wml1 chaetophrac
37	367	49.9	90	2 Q7YQJ8	Q7yqj8 vulpes vulp
38	367	49.9	89	2 Q8WML0	Q8wml0 nephtitis me
39	361	49.0	89	2 Q6YIR1	Q6yir1 ursus ameri
40	353	48.0	89	2 Q8WMK9	Q8wmk9 procyon lot
41	342	46.5	90	2 Q8WMK8	Q8wmk8 eptesicus f
42	340	46.2	86	2 Q8WJ10	Q8wj10 bos taurus
43	339.5	46.1	100	2 Q8UWJ3	Q8uwj3 gallus gall
44	330	44.8	90	2 Q7TMN1	Q7tmn1 castor cana
45	195	26.5	42	2 Q6QLP9	Q6qlp9 bos indicus

ALIGNMENTS

RESULT 1					
ID	OB_HUMAN	STANDARD;	PRT;	167 AA.	
DT	P41159; O15158;				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Leptin precursor (Obesity factor) (Obese protein).				
GN	Name=LEP; Synonyms=OB;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;				
RA	Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;				
RT	"Positional cloning of the mouse obese gene and its human homologue.";				
RL	Nature 372:425-432(1994).				
RN	[2]				
RP	ERRATUM.				
RA	Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;				
RL	Nature 374:479-479(1995).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95309556; PubMed=7789654;				
RA	Masuzaki H., Ogawa Y., Isse N., Satoh N., Okazaki T., Shigemoto M.,				
RA	Mori K., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,				
RA	Nakao K.;				
RT	"Human obese gene expression. Adipocyte-specific expression and				
RT	regional differences in the adipose tissue.";				
RL	Diabetes 44:855-858(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96223958; PubMed=8626726; DOI=10.1074/jbc.271.8.3971;				
RA	Gong D.W., Bi S., Pratley R.E., Weintraub B.D.;				
RT	"Genomic structure and promoter analysis of the human obese gene.";				
RL	J. Biol. Chem. 271:3971-3974(1996).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RA	Chehab F.F., Lim M.E.;				
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96070903; PubMed=7499240; DOI=10.1074/jbc.270.46.27728;				
RA	Isse N., Ogawa Y., Tamura N., Masuzaki H., Mori K., Okazaki T.,				
RA	Satoh N., Shigemoto M., Yoshimasa Y., Nishi S., Hosada K., Inazawa J.,				
RA	Nakao K.;				
RT	"Structural organization and chromosomal assignment of the human obese				
RT	gene.";				
RL	J. Biol. Chem. 270:27728-27733(1995).				
RN	[7]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96198511; PubMed=8621021;				

RA Niki T., Mori H., Tamori Y., Kishimoto-Hashimoto M., Ueno H.,
RA Araki S., Masugi J., Sawant N., Majithia H.R., Rais N.,
RA Hashimoto M., Taniguchi H., Kasuga M.,
RT "Human obese gene: molecular screening in Japanese and Asian Indian
RL NIDDM patients associated with obesity.";
RN Diabetes 45:675-678(1996).
RP SEQUENCE FROM N.A.
RL Lu L., Fu Z., Xu M., Fu Y., Hu Z.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RN and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN INTERACTION WITH SIGLEC6.
RX MEDLINE=99357812; PubMed=10428856; DOI=10.1074/jbc.274.32.22729;
RA Patel N., Brinkman-Van der Linden E.C.M., Altman S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.;
RT "OB-RP1/Siglec-6. A leptin- and sialic acid-binding protein of the
RN immunoglobulin superfamily.";
RL J. Biol. Chem. 274:22729-22738(1999).
RN ERRATUM.
RA Patel N., Brinkman-Van der Linden E.C.M., Altman S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.;
RN J. Biol. Chem. 274:28058-28058(1999).
RN STRUCTURE BY NMR.
RX MEDLINE=97309492; PubMed=9166907; DOI=10.1016/S0014-5793(97)00353-0;
RA Kline A.D., Becker G.W., Churgay L.M., Landen B.E., Martin D.K.M.,
RA Muth W.L., Rathnachalam R., Richardson J.M., Schoner B., Ulmer M.,
RA Hale J.B.;
RT "Leptin is a four-helix bundle: secondary structure by NMR.";
RL FEBS Lett. 407:239-242(1997).
RN [13]
RX X-RAY CRYSTALLOGRAPHY (2.4 ÅNGSTROMS).
RA Zhang F., Basinski M.B., Beals J.M., Briggs S.L., Churgay L.M.,
RA Clawson D.K., Dimarchi R.D., Furman T.C., Hale J.E., Heitung H.M.,
RA Schoner B.E., Smith D.P., Zhang X.Y., Wery J.P., Schervitz R.W.;
RT "Crystal structure of the obese protein leptin-B100.";
RL Nature 387:206-209(1997).
RN [14]
RP VARIANT MET-94.
RA Bartholomew D.W., McClellan J.M.;
RT "A novel polymorphism in the leptin gene.";
RL Hum. Mutat. 12:220-220(1998).
RN [15]
RP VARIANT MORBID OBESITY TEP-105.
RX MEDLINE=98160176; PubMed=9500540;

Strobel A., Issad T., Camoin L., Ozata M., Strosberg A.D.;
"A leptin missense mutation associated with hypogonadism and morbid
obesity.";
Nat. Genet. 18:213-215(1998).
-!- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass.
-!- SUBUNIT: Interacts with SIGLEC6.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DISEASE: Defects in LEP may be a cause of autosomal recessive
obesity [MIM:601665].
-!- SIMILARITY: Belongs to the leptin family.
-!- DATABASE: NAME=RAID Systems' cytokine mini-reviews: LEP;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=213".
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EMBL; U18915; AAA60470.1; -;
EMBL; D49487; BAA08448.1; -;
EMBL; U43653; AAC50400.1; -;
EMBL; U43415; AAC31660.1; -;
EMBL; D63710; BAA09839.1; -;
EMBL; D63709; BAA09839.1; JOINED..
EMBL; D63519; BAA09787.1; -;
EMBL; D63518; BAA09787.1; JOINED.
EMBL; AF008123; AAB63507.1; -;
EMBL; BC060830; AAB60830.1; -;
PIR; A38952; LTHU.
PIR; I53166; I53166.
PDB; 1AX8; X-ray; @=22-167.
Genew; HGNC:6553; LEP.
MIM; 164160; -;
MIM; 601665; -;
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0006112; P:energy reserve metabolism; TAS.
InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR000065; Leptin.
Pfam; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
3D-structure; Diabetes mellitus; Disease mutation; Obesity;
Polymorphism; Signal.
SIGNAL 1 21 Potential.
CHAIN 22 167 Leptin.
DISULFID 117 167
VARIANT 49 49 Missing (in 30% the clones).
VARIANT 94 94 V -> M.
VARIANT 105 105 /FTID=VAR_004197.
VARIANT 110 110 R -> W (in morbid obesity and
hypoconadism).
VARIANT 110 110 /FTID=VAR_008094.
CONFLICT 96 V -> M (in dbSNP:1800564).
HELEX 25 44 /FTID=VAR_011955.
HELEX 72 87 Q -> R (in Ref. 8).
TURN 88 88
TURN 92 114
TURN 115 116
HELEX 128 131
HELEX 132 135
STRAND 137 137
TURN 138 139
STRAND 140 140

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Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
Qy 61 YQQLITSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQQLITSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLSQDMLWQLDLSGPC 146

RESULT 4
OB GORGO
ID OB GORGO STANDARD; PRT; 146 AA.
AC Q95189;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.P., Zhang X., Hsiung H.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U72872; AAB17091.1; -.
CC HSP; P41159; IAX8.
CC InterPro; IPR009079; 4_helix_cytokine.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC Obesity.
CC DISULFID 96 146 By similarity.
CC SEQUENCE 146 AA; 16031 MW; 02C43BF6B9A4C85C CRC64;
CC
CC Query Match 98.9%; Score 728; DB 1; Length 146;
CC Best Local Similarity 98.6%; Pred. No. 5e-59;
CC Matches 144; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC
CC 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
CC 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
CC 61 YQQLITSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
CC 61 YQQLITSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
CC 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
CC 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
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RESULT 5
OB PONPY
ID OB PONPY STANDARD; PRT; 146 AA.
AC Q95234;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RA Rockey P.K., Rostek P.R.;
RT "Cloning of obese genes from different species: a comparison of the
RT gene structures and the sequences of the obese gene products,
RT leptin.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U72873; AAB17092.1; -.
CC HSP; P41159; IAX8.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR000065; Leptin.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC Obesity.
CC DISULFID 96 146 By similarity.
CC SEQUENCE 146 AA; 16195 MW; 3F50A13338FPDBD4 CRC64;
CC
CC Query Match 98.0%; Score 721; DB 1; Length 146;
CC Best Local Similarity 97.3%; Pred. No. 2.2e-58;
CC Matches 142; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
CC
CC 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
CC 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
CC 61 YQQLITSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
CC 61 YQQLITSPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
CC 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
CC 121 TEVALSRLOGLSQDMLWQLDLSGPC 146

RESULT 6
OB MACMU
ID OB MACMU STANDARD; PRT; 167 AA.
AC Q28504;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
```

FT HELIX 142 160
FT HELIX 161 163

Query Match 100.0%; Score 736; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|||
Db 22 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
|||

QY 61 YQOILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
|||
Db 82 YQOILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 141
|||

QY 121 TEVVALSRLOGLQDMLWQDLSPGC 146
|||
Db 142 TEVVALSRLOGLQDMLWQDLSPGC 167
|||

RESULT 2

OB PANTR PRELIMINARY; PRT; 167 AA.

AC Q6NT58
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Leptin.
GN Name=LEP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RESULT 3

OB PANTR STANDARD; PRT; 146 AA.

AC Q02750;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RA Rockey P.K., Rostock P.R.;
RT "Cloning of obese genes from different species: a comparison of the
gene structures and the sequences of the obese gene products,
leptin."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; U96450; AAB54023.1; -.
DR HSP; P41159; IAX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
SQ SEQUENCE 146 AA; 16058 MW; 02C42A06B554D55C CRC64;

Query Match 99.6%; Score 733; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.7e-59;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|||

DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RA MEDLINE=96411743; PubMed=8810296; DOI=10.1074/jbc.271.41.25327;
RX Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Nicolson M.A.,
RA Hansen B.C.;
RT "Regulation of obese (ob) mRNA and plasma leptin levels in rhesus
monkeys. Effects of insulin, body weight, and non-insulin-dependent
diabetes mellitus."
RL J. Biol. Chem. 271:25327-25331(1996).
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC -----
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CC -----
DR EMBL; U58492; AAC50730.1; -
DR HSSP; P41159; IAX8.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR PRODOM; PD005698; Leptin; 1.
KW Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT SEQUENCE 167 AA; 18953 MW; E7D9F30628A5BB99 CRC64;
Query Match 91.3%; Score 672; DB 1; Length 167;
Best Local Similarity 91.1%; Pred. No. 8.4e-54;
Matches 133; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
DB 22 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAI 81
QY 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 82 YQQLTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141
QY 121 TEVVALSRQGLQDMLWQLDLSGPC 146
DB 142 TEVVALSRQGLQDMLWQLDLSGPC 167
RESULT 7
OB FELCA STANDARD; PRT; 167 AA.
AC Q9N2C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=White adipose tissue;
RA Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
RT "Molecular cloning of feline leptin cDNA."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC -----
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CC -----
DR EMBL; AB041360; BAA95481.1; -
DR HSSP; P41159; IAX8.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR PRODOM; PD005698; Leptin; 1.
KW Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT SEQUENCE 167 AA; 18583 MW; 643720DBB0AB4B95 CRC64;
Query Match 86.8%; Score 639; DB 1; Length 167;
Best Local Similarity 86.3%; Pred. No. 9e-51;
Matches 126; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
DB 22 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAI 81
QY 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 82 YQQLTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141
QY 121 TEVVALSRQGLQDMLWQLDLSGPC 146
DB 142 TEVVALSRQGLQDMLWQLDLSGPC 167
RESULT 8
Q6T8R8 PRELIMINARY; PRT; 146 AA.
ID Q6T8R8
AC Q6T8R8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leptin (Fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RA Rajendran S., Shukla D.C., Saravanan B.C.;

```

Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY427959; AAB05862.1;
DR HSP: P41159; IAX8
DR GO: GO:0005576; C:extracellular; IEA
DR GO: GO:0005179; F:hormone activity; IEA
DR GO: GO:0007165; P:signal transduction; IEA
DR InterPro: IPR009079; 4 helix_cytokine.
DR InterPro: IPR000065; Leptin.
DR Pfam: PF02024; Leptin.
DR PRINTS: PR00495; LEPTIN.
DR ProDom: PD005698; Leptin; 1.
FT CHAIN 1 146 leptin.
FT NON_TER <1 146
SQ SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;

Query Match 85.3%; Score 628; DB 2; Length 146;
Best Local Similarity 87.0%; Pred. No. 7.8e-50;
Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPQIKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
Db 1 VPIRKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAI 60

QY 61 YQQLTSPMRNVQISNDLENLRLDLHLVAFKSKCHLPWASGLTDLSCGVLEASGYS 120
Db 61 YQQLTSLPSRVVQISNDLENLRLDLHLVAFKSKCHLPQVRALESLSGVLEASLYS 120

QY 121 TEVALSRLOGSQDMLQDLSPGC 146
Db 121 TEVALSRLOGSQDMLQDLSPGC 146

RESULT 9
OB BOVIN
ID OB BOVIN STANDARD; PRT; 167 AA
AC P05095; Q97918; Q95133; Q9TS29;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB, OBS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Tellam R.L., Briscoe S., Vuocolo A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 22-167 FROM N.A.
RA Ji S., Spurlock M.E.;
RL "Partial cloning of bovine obesity gene.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 22-167 FROM N.A.
RC TISSUE=white adipose tissue;
RA Kawakita Y., Abe H., Miyashige T.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS CYS-25 AND VAL-80.
RC STRAIN=Jersey;
RX MEDLINE=20063685; PubMed=10594237;
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Resequencing of DNA from a diverse panel of cattle reveals a high
RL level of polymorphism in both intron and exon.";
RL Mamm. Genome 10:1142-1145(1999).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT CYS-25.
RA Liefers S.C.;
RT "Genotype effects of bovine leptin mutations on pre- and postpartum
leptin concentrations.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 46-145 FROM N.A.
RA Lien S., Sundvold H., Klungland H., Vaegre D.I.;
RT "Two novel polymorphisms in the bovine obesity gene (OBS).";
RL Anim. Genet. 28:245-245(1997).
RN [7]
RP SEQUENCE OF 60-146 FROM N.A.
RX MEDLINE=96269621; PubMed=8661738;
RA Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.;
RT "Chromosomal localization of the bovine obesity (OBS) gene.";
RL Mamm. Genome 7:398-399(1996).
RN [8]
RP SEQUENCE OF 1-48 FROM N.A.
RA Fitzsimmons C.J., Schmutz S.M.;
RT "Exon two of the bovine obese, leptin, gene.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC
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CC
EMBL: U43943; AAB85906.1;
EMBL: U50365; AAB61244.1;
EMBL: U85793; AAB06579.1;
EMBL: AB003143; BAA19750.1;
EMBL: AJ132764; CAB64255.1;
EMBL: AJ236854; CAB38018.1;
EMBL: AJ512638; CAD54745.1;
EMBL: AJ512639; CAD54745.1; JOINED.
EMBL: Y11369; CAA72197.1;
EMBL: U43833; AAB18762.1;
EMBL: AF120500; AAD23567.1;
HSP: P41159; IAX8.
InterPro: IPR009079; 4 helix_cytokine.
Pfam: PF02024; Leptin.
PRINTS: PR00495; LEPTIN.
ProDom: PD005698; Leptin; 1.
Obesity; Polymorphism; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT VARIANT 25 25 R -> C.
FT VARIANT 80 80 A -> V.
FT CONFLICT 25 25 R -> Q (in Ref. 2).
FT CONFLICT 166 166 G -> E (in Ref. 2).
SQ SEQUENCE 167 AA; 18716 MW; 94C666B3069E50B7 CRC64;

Query Match 85.3%; Score 628; DB 1; Length 167;
Best Local Similarity 87.0%; Pred. No. 9.3e-50;
Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPQIKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
Db 22 VPIRKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAI 81

QY 61 YQQLTSPMRNVQISNDLENLRLDLHLVAFKSKCHLPWASGLTDLSCGVLEASGYS 120
Db 82 YQQLTSLPSRVVQISNDLENLRLDLHLVAFKSKCHLPQVRALESLSGVLEASLYS 141
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Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY427959; AAR05862.1; -
 DR HSSP; P41159; IAX8.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR Pfam; PF02024; Leptin.
 DR PRINTS; PR00495; Leptin.
 DR ProDom; PD005698; Leptin.
 DR NON TER 1 1
 FT CHAIN 1 146
 SQ SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;
 Query Match 85.3%; Score 628.1; Def 2; Length 146;
 Best Local Similarity 87.0%; Pred. No. 7.8e-50;
 Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQVGLDFPGLHPLLSKMDQTLAI 60
 Db 1 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQVGLDFPGLHPLLSKMDQTLAI 60
 QY 61 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLDSLGVLASGYS 120
 Db 61 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLDSLGVLASGYS 120
 QY 121 TEVALSRLOGLSLODMQLDLSFGC 146
 Db 121 TEVALSRLOGLSLODMQLDLSFGC 146

RESULT 9

OB BOVIN
 ID OB_BOVIN
 AC P50595; O97918; STANDARD; PRT; 167 AA.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 25-OCT-1996 (Rel. 34, Last sequence update)
 DE Leptin precursor (Obesity factor).
 GN Names:LEP; Synonyms:OB, OBS;
 OS Bos taurus (Bovine)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX NCBI_TaxID=9913;
 RP [1]
 RC TISSUE=Liver;
 RA Talam R.L., Briscoe S., Vuocolo A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 22-167 FROM N.A.
 RA Ji S., Spurlock M.E.;
 RL "Partial cloning of bovine obesity gene";
 RN Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP SEQUENCE OF 22-167 FROM N.A.
 RC TISSUE=White adipose tissue;
 RA Kawakita Y., Abe H., Miyashige T.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS CYS-25 AND VAL-80.
 RC STRAIN=Jersey;
 RX MEDLINE=20063685; PubMed=10594237;
 RA Konfortov B.A., Licence V.E., Miller J.R.;
 RT "Resequencing of DNA from a diverse panel of cattle reveals a high level of polymorphism in both intron and exon.";
 RL Mamm. Genome 10:1142-1145 (1999).
 RP [5]
 RA SEQUENCE FROM N.A., AND VARIANT CYS-25.
 RL Liefers S.C.;
 RT "Genotype effects of bovine leptin mutations on pre- and postpartum

leptin concentrations.";
 RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 46-145 FROM N.A.
 RA Lien S., Sundvold H., Klungland H., Vaege D.I.;
 RL "Two novel polymorphisms in the bovine obesity gene (OBS).";
 RN Anim. Genet. 28:245-245 (1997).
 RP [7]
 RP SEQUENCE OF 60-146 FROM N.A.
 RA MEDLINE=96269621; PubMed=8661738;
 RL Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.;
 RN Mamm. Genome 7:398-399 (1996).
 RP [8]
 RP SEQUENCE OF 1-48 FROM N.A.
 RA Fitzsimmons C.J., Schmutz S.M.;
 RL "Exon two of the bovine obese, leptin, gene.";
 RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
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 DR EMBL; U43943; AAA85906.1;
 DR EMBL; U50365; AAB61244.1;
 DR EMBL; U65793; AAB06579.1;
 DR EMBL; AB003143; BAA19750.1;
 DR EMBL; AJ132764; CAB64255.1;
 DR EMBL; AJ236854; CAB38018.1;
 DR EMBL; AJ512638; CAD54745.1;
 DR EMBL; AJ512639; CAD54745.1;
 DR EMBL; Y11369; CA72197.1;
 DR EMBL; U43833; AAB18762.1;
 DR EMBL; AF120500; AAD23567.1;
 DR HSSP; P41159; IAX8.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR Pfam; PF02024; Leptin.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin.
 KW Obesity; Polymorphism; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 FT VARIANT 25 25 R -> C.
 FT CONFLICT 80 80 A -> V.
 FT CONFLICT 25 25 R -> Q (in Ref. 2).
 FT CONFLICT 166 166 G -> E (in Ref. 2).
 SQ SEQUENCE 167 AA; 18716 MW; 94C66B83069E50B7 CRC64;
 Query Match 85.3%; Score 628; DB 1; Length 167;
 Best Local Similarity 87.0%; Pred. No. 9.3e-50;
 Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQVGLDFPGLHPLLSKMDQTLAI 60
 Db 1 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQVGLDFPGLHPLLSKMDQTLAI 60
 QY 61 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLDSLGVLASGYS 120
 Db 61 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLDSLGVLASGYS 120
 QY 82 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLDSLGVLASGYS 141
 Db 82 YQIILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLDSLGVLASGYS 141

121 TEVVALSRLQSLQDMLWQLDLSPGC 146
 142 TEVVALSRLQSLQDMLWQLDLSPGC 167

RESULT 10

OB_PIG OB_PIG STANDARD; PRT; 167 AA.

QY Q29406; O19095; Q95251; PRT; 167 AA.
 DB 01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 25-OCT-2004 (Rel. 45, Last annotation update)
 Leptin precursor (Obesity factor).
 Name=LEP; Synonyms=OB, OBS;
 Sus scrofa (Pig).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 [1]
 SEQUENCE FROM N.A.
 RC TISSUE=Adipose tissue;
 RA Louis C.F.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A.
 RP Ramsay T.G., Yan X.;
 RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 RP STRAIN=Landrace;
 RC Robert C., Palin M.-F., Coulombe N., Roberge C., Silversides F.G.,
 RA Benkel B.F., McKay R.M., Pelletier G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 [4]
 SEQUENCE FROM N.A.
 RP Bidwell C.A., Ji S., Spurlock M.E.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 RP STRAIN=Meishan;
 RC Dai R., Li N., Hu X., Wu C.;
 RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 [6]
 SEQUENCE FROM N.A.
 RP McNeel R.L., Mergmann H.J.;
 RL "Adipose tissue regulatory transcript expression in lean versus obese
 pigs.";
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 [7]
 SEQUENCE FROM N.A.
 RP STRAIN=Large white;
 RC Soares M.A.M., Euclides R.F., Guimaraes S.E.F., Martins M.F.,
 RA Lopes P.S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 [8]
 SEQUENCE OF 15-110 FROM N.A.
 RP TISSUE=White adipose tissue;
 RC MEDLINE=97009821; PubMed=8856925;
 RX Neuenschwander S., Rettenberger G., Meijerink E., Jorg H.,
 RA Stranzinger G.;
 RL "Partial characterization of porcine obesity gene (OBS) and its
 localization to chromosome 18 by somatic cell hybrids.";
 RT Anim. Genet. 27:275-278 (1996).
 RT

-!- FUNCTION: May function as part of a signaling pathway that acts to
 regulate the size of the body fat depot. An increase in the level
 of LEP may act directly or indirectly on the CNS to inhibit food
 intake and/or regulate energy expenditure as part of a homeostatic
 mechanism to maintain constancy of the adipose mass.
 CC

-!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC

-!- SIMILARITY: Belongs to the leptin family.
 CC

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Domest. Anim. Endocrinol. 14:295-303(1997).
 -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.
 -!- SUBCELLULAR LOCATION: Secreted (Probable).
 -!- SIMILARITY: Belongs to the leptin family.

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 EMBL; U84247; AB41786.1; -;
 EMBL; U62123; AB51033.1; -;
 HSSP; P41159; IAX8.
 InterPro; IPR009079; 4_helix_cytokine.
 Pfam; PF02024; Leptin; 1.
 PRINTS; PR00495; LEPTIN.
 PRODOM; PD005698; Leptin; 1.
 Obesity.
 FT DISULFID 96 146 By similarity.
 FT CONFLICT 65 65 L -> H (in Ref. 2).
 FT CONFLICT 92 92 A -> G (in Ref. 2).
 FT CONFLICT 124 124 V -> L (in Ref. 2).
 SQ SEQUENCE 146 AA; 16053 MW; 19D54C53240968CA CRC64;
 Query Match 84.8%; Score 624; DB 1; Length 146;
 Best Local Similarity 87.0%; Pred. No. 1.8e-49;
 Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQVTVGLDPIGLHPILTLKMDQTLAV 60
 Db 1 VPIRQVDDTKTLIKTIVTRINDISHTQSVSSKQVTVGLDPIGLHPILTLKMDQTLAI 60
 Qy 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCPLPWASGLTDLSDLGVLASGYS 120
 Db 61 YQQLIASLPSRNVIQISNDLENLRLDLHLVLAFAKSCPLPWRALESLSLGVLASLYS 120
 Qy 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 Db 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 RESULT 12
 OB MOUSE STANDARD; PRT; 167 AA.
 AC P41160;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=Lept; Synonym=Ob;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;
 RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
 RT "Positional cloning of the mouse obese gene and its human homologue";
 RL Nature 372:425-432(1994).
 RN [2]
 RP ERRATUM.
 RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
 RL Nature 374:479-479(1995).
 RN [3]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Chehab F.F., Lim M.E.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- DISEASE: Defects in LEP are the cause of profound obesity and type II diabetes.
 CC -!- SIMILARITY: Belongs to the leptin family.

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 EMBL; U18812; AAA64564.1; -;
 EMBL; U22421; AAA64213.1; -;
 PIR; S50863; LTWS.
 HSSP; P41159; IAX8.
 MGD; MGI:104663; Lep.
 GO; GO:0008083; F; Growth factor activity; IDA.
 GO; GO:0005515; F; Protein binding; IPI.
 GO; GO:0008206; P; Bile acid metabolism; IDA.
 GO; GO:0045639; P; Positive regulation of myeloid blood cell d. . .; IDA.
 GO; GO:0030300; P; Regulation of cholesterol absorption; IDA.
 InterPro; IPR009079; 4_helix_cytokine.
 InterPro; IPR000065; Leptin.
 Pfam; PF02024; Leptin; 1.
 PRINTS; PR00495; LEPTIN.
 PRODOM; PD005698; Leptin; 1.
 KW Diabetes mellitus; Obesity; Signal.
 FT SIGNAL 1 21 potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 FT VARIANT 49 49 Missing (in 30% the clones).
 SQ SEQUENCE 167 AA; 18708 MW; D6783B6C76FD7116 CRC64;
 Query Match 84.1%; Score 619; DB 1; Length 167;
 Best Local Similarity 84.9%; Pred. No. 6.2e-49;
 Matches 124; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQVTVGLDPIGLHPILTLKMDQTLAV 60
 Db 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSAQRVTGLDPIGLHPILTLKMDQTLAV 81
 Qy 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCPLPWASGLTDLSDLGVLASGYS 120
 Db 82 YQQLVTLSPSNVLIQISNDLENLRLDLHLVLAFAKSCPLPOTSGLOKPSLDGVLASLYS 141
 Qy 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 Db 142 TEVVALSRQGSQDMLWQLDLSFGC 167
 RESULT 13
 OB RAT STANDARD; PRT; 167 AA.
 ID AC P50596;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=Lept; Synonym=Ob;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=95386724; PubMed=7657834;
 RA Ogawa Y., Masuzaki H., Isse N., Okazaki T., Mori K., Shigemoto M.,
 RA Satoh N., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,
 RA Nakao K.;
 RN "Molecular cloning of rat obese cDNA and augmented gene expression in
 RT genetically obese Zucker fatty (fa/fa) rats.";
 RL J. Clin. Invest. 96:1647-1652(1995).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Fat;
 RX MEDLINE=95314614; PubMed=7794258;
 RA Funahashi T., Shimomura I., Hiraoka H., Arai T., Takahashi M.,
 RA Nakamura T., Nozaki S., Yamashita S., Takemura K., Tokunaga K.,
 RN "Enhanced expression of rat obese (ob) gene in adipose tissues of
 RT ventromedial hypothalamus (VMH)-lesioned rats.";
 RL Biochem. Biophys. Res. Commun. 211:469-475(1995).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Leto, Oletif, and Zucker; TISSUE=Adipose tissue;
 RX MEDLINE=95251725; PubMed=7733988;
 RA Murakami T., Shima K.;
 RN "Cloning of rat obese cDNA and its expression in obese rats.";
 RL Biochem. Biophys. Res. Commun. 209:944-952(1995).
 [4]
 RN SEQUENCE OF 14-167 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Fat;
 RX Submitted P.A., Sivitz W.I., Bailey H.L.;
 RA Donohoue P.A., Sivitz W.I., Bailey H.L.;
 RN Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of Lep may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: Belongs to the leptin family.
 CC
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 CC
 CC EMBL; D45862; BAA08296.1; -;
 CC EMBL; S78586; AAB34657.2; -;
 CC EMBL; D49653; BAA08529.1; -;
 CC EMBL; U48849; AAC52514.1; -;
 CC PIR; PC4034; LTRT.
 CC HSP; P41159; IAX8.
 CC RGD; 3000; Lep.
 CC InterPro; IPR009079; 4_helix_cytokine.
 CC InterPro; IPR000065; Leptin.
 CC Pfam; PF02024; Leptin; 1.
 CC PRINTS; PR00495; LEPTIN.
 CC ProDom; PD005698; Leptin; 1.
 CC Obesity; Signal.
 KW SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 FT CONFLICT 32 32 K -> T (in Ref. 2).
 FT CONFLICT 163 163 L -> V (in Ref. 4).
 SQ SEQUENCE 167 AA; 18866 MW; 385B563DA42EC84E CRC64;
 Query Match 82.2%; Score 605; DB 1; Length 167;
 Best Local Similarity 83.6%; Pred. No. 1.2e-47;
 Matches 122; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
 Qy 1 VPIQKQVDDTKTLIKTIVTRINDISHTSQSVSSKQKVTGLDIPGLHPIILSKMDQTLAV 60

Db 22 VPIHKVDDTKTLIKTIVTRINDISHTSQSVSSKQKVTGLDIPGLHPIILSKMDQTLAV 81
 Qy 61 YQIILTSMPSRNVIQISNDLENLRDLHLVLAFLAKSCHLPWASGLTLDLGGVLEASGYS 120
 Db 82 YQIILTSMPSRNVIQIHAHLENLRDLHLVLAFLAKSCHLPWASGLTLDLGGVLEASGYS 141
 Qy 121 TEVVALSRLOGLSLODMWLDLSPGC 146
 Db 142 TEVVALSRLOGLSLODMWLDLSPGC 167
 RESULT 14
 ID OB CANFA STANDARD; PRT; 167 AA.
 AC 002720; Q9TSG1;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=Lep; Synonyms=OB;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=White adipose tissue;
 RA Iwase M., Sasaki N., Komagome R., Kimura K., Saito M.;
 RN "Molecular cloning of canine leptin cDNA.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE OF 22-167 FROM N.A.
 RC TISSUE=Adipose tissue;
 RA Smith D.P., Zhang X., Hsiung H.M.;
 RN Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of Lep may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: Belongs to the leptin family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB020986; BAA35129.1; -;
 CC EMBL; U95642; AAB53654.1; -;
 CC HSP; P41159; IAX8.
 CC InterPro; IPR009079; 4_helix_cytokine.
 CC InterPro; IPR000065; Leptin.
 CC Pfam; PF02024; Leptin; 1.
 CC PRINTS; PR00495; LEPTIN.
 CC ProDom; PD005698; Leptin; 1.
 CC Obesity; Signal.
 KW SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 FT CONFLICT 148 148 N -> S (in Ref. 2).
 SQ SEQUENCE 167 AA; 18654 MW; 9703CFBED2286A55 CRC64;
 Query Match 81.0%; Score 596; DB 1; Length 167;
 Best Local Similarity 82.2%; Pred. No. 8.1e-47;
 Matches 120; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
 Qy 1 VPIQKQVDDTKTLIKTIVTRINDISHTSQSVSSKQKVTGLDIPGLHPIILSKMDQTLAV 60

Db	22	VPIRVQDDTKTLIKTIIVARINDISHTQSVSSKQVAGLDFIPGLQVLSLRMDQTLAI	81	Matches	120;	Conservative	13;	Mismatches	12;	Indels	1;	Gaps	1;
Qy	61	YQOILTSMPNRVNIQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGVLEASGYS	120										
Db	82	YQOILNLSHSRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGVLEASGYS	141										
Qy	121	TEVVALSRLOGLQSLQDMLWQLDLSFGC	146										
Db	142	TEVVALNRLQALQDMLRRLDLSFGC	167										

RESULT 15

OB_CHICK	OB_CHICK	STANDARD;	PRT;	163	AA.
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AC	047164;				
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	25-OCT-2004	(Rel. 45, Last annotation update)			
DE	Leptin precursor (Obesity factor).				
GN	Name=LEP; Synonyms=OB;				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Broiler; TISSUE=Liver;				
RX	MEDLINE=98201619; PubMed=9524275; DOI=10.1016/S0378-1119(97)00670-7;				
RA	Tacuis M., Chen J.W., Daviaud C., Dupont J., Derouet M., Simon J.;				
RT	"Cloning the chicken leptin gene.";				
RL	Gene 208:239-242(1998).				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Shaver; TISSUE=Adipose tissue, and Liver;				
RA	Ashwell C.M., Czerwinski S.M., McMurtry J.P.;				
RL	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: May function as part of a signaling pathway that acts to				
CC	regulate the size of the body fat depot. An increase in the level				
CC	of LEP may act directly or indirectly on the CNS to inhibit food				
CC	intake and/or regulate energy expenditure as part of a homeostatic				
CC	mechanism to maintain constancy of the adipose mass (By				
CC	similarity).				
CC	-1- SUBCELLULAR LOCATION: Secreted (Probable).				
CC	-1- TISSUE SPECIFICITY: Not exclusively localized in adipose tissue				
CC	but is also expressed in liver.				
CC	-1- SIMILARITY: Belongs to the leptin family.				

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CC	EMBL; AF012727; AAC60368.1; -;				
DR	EMBL; AF082500; AAC32380.1; -;				
DR	HSSP; P41159; IAX8.				
DR	InterPro; IPR009079; 4_helix_cytokine.				
DR	InterPro; IPR000065; Leptin.				
DR	Pfam; PF02024; Leptin; 1.				
DR	PRINTS; PR00495; LEPTIN.				
DR	ProDom; PD005698; Leptin; 1.				
KW	Obesity; Signal.				
FT	SIGNAL	1	18	Potential.	
FT	CHAIN	19	163	Leptin.	
FT	DISULFID	113	163	By similarity.	
SQ	SEQUENCE	163	AA;	18183	MW; 9F578DB2528B18FC

Query Match 79.7%; Score 586.5; DB 1; Length 163;
Best Local Similarity 82.2%; Pred. NO. 5.9e-46;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:33 ; Search time 32.5463 Seconds
(without alignments)
383.035 Million cell updates/sec

Title: US-10-049-182-4

Perfect score: 870

Sequence: 1 MHWTGCGFLWLPYLFVYQ.....SRQGSLOQLMWQLDLSFGC 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pap:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	167	2	US-08-540-242A-4
2	870	100.0	167	2	US-08-347-563A-4
3	870	100.0	167	2	US-09-003-081-5
4	870	100.0	167	3	US-08-292-345B-4
5	870	100.0	167	3	US-08-648-262-5
6	870	100.0	167	3	US-08-648-263-5
7	870	100.0	167	3	US-08-485-942A-4
8	870	100.0	167	3	US-08-488-214A-4
9	870	100.0	167	3	US-08-488-208A-4
10	870	100.0	167	3	US-08-759-628-1
11	870	100.0	167	3	US-08-688-908-7
12	870	100.0	167	3	US-08-483-211A-4
13	870	100.0	167	3	US-08-488-223A-4
14	870	100.0	167	3	US-09-147-805-4
15	870	100.0	167	4	US-08-438-431A-4
16	870	100.0	167	4	US-08-488-225A-4
17	870	100.0	167	4	US-09-204-730B-4
18	870	100.0	167	4	US-09-316-393-4
19	870	100.0	167	4	US-09-377-081-17
20	870	100.0	167	4	US-09-686-647A-4
21	870	100.0	167	5	PCT-US96-01471-4
22	870	100.0	397	4	US-08-775-066-2
23	854.5	98.2	166	2	US-08-347-563A-6
24	854.5	98.2	166	2	US-08-292-345B-6
25	854.5	98.2	166	3	US-08-485-942A-6
26	854.5	98.2	166	3	US-08-488-214A-6
27	854.5	98.2	166	3	US-08-488-208A-6

28 854.5 98.2 166 3 US-08-483-211A-6 Sequence 6, Appli
29 854.5 98.2 166 3 US-08-488-223A-6 Sequence 6, Appli
30 854.5 98.2 166 4 US-08-438-431A-6 Sequence 6, Appli
31 854.5 98.2 166 4 US-08-488-225A-6 Sequence 6, Appli
32 854.5 98.2 166 4 US-09-204-730B-6 Sequence 6, Appli
33 854.5 98.2 166 4 US-09-316-393-6 Sequence 6, Appli
34 854.5 98.2 166 4 US-09-686-647A-6 Sequence 6, Appli
35 736 84.6 146 1 US-08-398-021-3 Sequence 3, Appli
36 736 84.6 146 2 US-08-788-943A-5 Sequence 3, Appli
37 736 84.6 146 2 US-08-823-104-3 Sequence 3, Appli
38 736 84.6 146 2 US-09-003-081-6 Sequence 6, Appli
39 736 84.6 146 3 US-08-648-262-6 Sequence 6, Appli
40 736 84.6 146 3 US-08-648-263-6 Sequence 6, Appli
41 736 84.6 146 3 US-08-914-375C-32 Sequence 32, Appli
42 736 84.6 146 4 US-09-172-644-1 Sequence 1, Appli
43 736 84.6 146 4 US-09-221-178-1 Sequence 1, Appli
44 736 84.6 146 4 US-09-200-919-1 Sequence 1, Appli
45 736 84.6 146 5 PCT-US96-00952-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-540-242A-4

; Sequence 4, Application US/08540242A

; Patent No. 5827734

; GENERAL INFORMATION:

; APPLICANT: Weigle, David S.

; APPLICANT: Kuijper, Joseph L.

; APPLICANT: Forstrom, John W.

; APPLICANT: Lehner, Joyce M.

; TITLE OF INVENTION: APPETITE SUPPRESSION FACTOR AND RELATED METHODS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/540,242A

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Parker, Gary E

; REGISTRATION NUMBER: 31,648

; REFERENCE/DOCKET NUMBER: 95-01C5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6673

; TELEFAX: 206-442-6678

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 167 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-540-242A-4

Query Match 100.0%; Score 870; DB 2; Length 167;

Best Local Similarity 100.0%; Pred. No. 9.3e-88;

Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWTGCGFLWLPYLFVYQAVPIQKVQDDTKLTKIVTRINDISHTQSVSSKQKVTL 60

DB 1 MHWTGCGFLWLPYLFVYQAVPIQKVQDDTKLTKIVTRINDISHTQSVSSKQKVTL 60

QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLHLVLAFSKSHLP 120
Db |||||
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLSLODMLWQDLSPGC 167
Db |||||

RESULT 2

US-08-347-563A-4
; Sequence 4, Application US/08347563A
; Patent No. 5935810
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,563A
; FILING DATE: No. 5935810ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide
; ORIGINAL SOURCE: Human
US-08-347-563A-4

Query Match 100.0%; Score 870; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGTLGFLWLPYLFVQAVPIQKVQDDTKTIKTIVTRINDISHTQSVSSKQKVTGL 60
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Db |||||
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLSLODMLWQDLSPGC 167
Db |||||

RESULT 3

US-09-003-081-5
; Sequence 5, Application US/09003081
; Patent No. 5968779
; GENERAL INFORMATION:
; APPLICANT: Campfield, Arthur Dr.
; APPLICANT: Devos, Rene Dr.
; APPLICANT: Guisez, Yves Dr.
; TITLE OF INVENTION: Recombinant Obese (OB) Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche, Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,081
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/435,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Picut, Catherine A
; REGISTRATION NUMBER: 37419
; REFERENCE/DOCKET NUMBER: 9165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4387
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-09-003-081-5

Query Match 100.0%; Score 870; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGTLGFLWLPYLFVQAVPIQKVQDDTKTIKTIVTRINDISHTQSVSSKQKVTGL 60
Db |||||
QY 1 MHGTLGFLWLPYLFVQAVPIQKVQDDTKTIKTIVTRINDISHTQSVSSKQKVTGL 60
Db |||||
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLHLVLAFSKSHLP 120
Db |||||
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLHLVLAFSKSHLP 120
Db |||||
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLSLODMLWQDLSPGC 167
Db |||||

RESULT 4

US-08-292-345B-4
; Sequence 4, Application US/08292345B
; Patent No. 6001968
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 21

NAME: Kreisler, Lewis J
REGISTRATION NUMBER: 38522
REFERENCE/DOCKET NUMBER: RAN 4105/175-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4387
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-648-263-5

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHWGTLCGFLMWPLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLCGFLMWPLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
DB 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
QY 121 WASGLETLDSLGVLGVEASGYSTEVVALSRQSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDSLGVLGVEASGYSTEVVALSRQSLQDMLWQLDLSGPC 167

RESULT 7
US-08-485-942A-4
Sequence 4, Application US/08485942A
Patent No. 6048837
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE
TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
TITLE OF INVENTION: AMENDED)
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,942A
FILING DATE: JUNE 7, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: May 10, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: May 10, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide
ORIGINAL SOURCE: Human
US-08-485-942A-4

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHWGTLCGFLMWPLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLCGFLMWPLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
DB 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
QY 121 WASGLETLDSLGVLGVEASGYSTEVVALSRQSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDSLGVLGVEASGYSTEVVALSRQSLQDMLWQLDLSGPC 167

RESULT 8
US-08-488-214A-4
Sequence 4, Application US/08488214A
Patent No. 6124439
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE
TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
TITLE OF INVENTION: (AS AMENDED)
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,214A
FILING DATE: JUNE 7, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6124439ember 30, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide
ORIGINAL SOURCE: Human
US-08-488-214A-4

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVQISNDLENLRDLHLVLAFSKSHLP 120
Db 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVQISNDLENLRDLHLVLAFSKSHLP 120
Qy 121 WASGLETLDLSLGGVLEASGYSTEVVALSRQGSLODMLWQDLSPGC 167
Db 121 WASGLETLDLSLGGVLEASGYSTEVVALSRQGSLODMLWQDLSPGC 167

RESULT 9
US-08-488-208A-4
Sequence 4, Application US/08488208A
Patent No. 6124448
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klaubner & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,208A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6124448ember 30, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide
ORIGINAL SOURCE: Human
US-08-488-208A-4

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVQISNDLENLRDLHLVLAFSKSHLP 120
Db 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVQISNDLENLRDLHLVLAFSKSHLP 120
Qy 121 WASGLETLDLSLGGVLEASGYSTEVVALSRQGSLODMLWQDLSPGC 167
Db 121 WASGLETLDLSLGGVLEASGYSTEVVALSRQGSLODMLWQDLSPGC 167

RESULT 10
US-08-759-628-1
Sequence 1, Application US/08759628
Patent No. 6225446
GENERAL INFORMATION:
APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0552Q
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200

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; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
US-08-759-628-1

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Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels

QY	1	MHWGTLGFLMLWPVLFYQVAVPIQKVQDDTKTLKTIIVTRINDISHTQSVSSKQKVTL	60
Db	1	MHWGTLGFLMLWPVLFYQVAVPIQKVQDDTKTLKTIIVTRINDISHTQSVSSKQKVTL	60
QY	61	DFIPGLHPILTILSKMDQTLAVYQQIILTSMPSRVNIQISDNLENRLDLLHLVLAFAKSCHL	120
Db	61	DFIPGLHPILTILSKMDQTLAVYQQIILTSMPSRVNIQISDNLENRLDLLHLVLAFAKSCHL	120
QY	121	WASGLETLDLSLGGVLEASGYSTEVVALSRQGSIQDMLWQDLSPCC	167
Db	121	WASGLETLDLSLGGVLEASGYSTEVVALSRQGSIQDMLWQDLSPCC	167

RESULT 11
US-08-688-908-7
; Sequence 7, Application US/08688908
; Patent No. 6297027
; GENERAL INFORMATION:
; APPLICANT: Spurlock, Michael E.
; TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USES THEREOF

```

1 21P: 53202
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: Floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: PatentIn Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/08/688,908
16
17 FILING DATE: 31-JUL-1996
18
19 CLASSIFICATION: 435
20
21 ATTORNEY/AGENT INFORMATION:
22
23 NAME: Plotcher, Gary R.
24
25 REGISTRATION NUMBER: 27,830
26
27 REFERENCE/DOCKET NUMBER: PM-8808
28
29 TELECOMMUNICATION INFORMATION:
30
31 TELEPHONE: 414-273-2100
32
33 TELEFAX: 414-223-5000
34
35 INFORMATION FOR SEQ ID NO: 7:
36
37 SEQUENCE CHARACTERISTICS:
38
39 LENGTH: 167 amino acids
40
41 TYPE: amino acid
42
43 STRANDEDNESS:
44
45 TOPOLOGY: linear
46
47 MOLECULE TYPE: protein
48
49 US-08-688-908-7

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Query Match      100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MHWGTLGFLWLPYLFVQVAVPQKVQDDTKTKLTVTRINDISHTQSVSSKKQKVTGL 60

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61 DFTPLGLPIIITLSKMDQTLVAYQOILTSPMSRNVQISNDLENLRDLHLVAFSKSCHLP 120

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121 WASGLETLDSLGGVLEASGYSTEVVALSRQLGSLQDMLWQLDLSPGC 167

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; Sequence 4, Application US/08483211A
; Patent No. 6309853
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, C
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS,
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

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Query Match      100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MHWGTLGFLWLPYLFVQVPIQKVQDDTKTLTKTIVTRINDISHTQSVSSKQKVTGL 60
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DB 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDLENRLDLHLVLAFAFSKSCHLP 120
QY 121 WASGLETLDSLGGLVLEASGYSTEVVALSRLOGLSQDMLWQDLSPGC 167
DB 121 WASGLETLDSLGGLVLEASGYSTEVVALSRLOGLSQDMLWQDLSPGC 167

RESULT 13
US-08-488-223A-4
; Sequence 4, Application US/08488223A
; Patent No. 6350730
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THE
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,223A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,943
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6350730ember 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-488-223A-4

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHWGTLGFLWLPYLFVQVPIQKVQDDTKTLTKTIVTRINDISHTQSVSSKQKVTGL 60
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QY 121 WASGLETLDSLGGLVLEASGYSTEVVALSRLOGLSQDMLWQDLSPGC 167
DB 121 WASGLETLDSLGGLVLEASGYSTEVVALSRLOGLSQDMLWQDLSPGC 167
RESULT 14
US-09-147-805-4
; Sequence 4, Application US/09147805
; Patent No. 6399745
; GENERAL INFORMATION:
; APPLICANT: ERTL, Johann
; PREIBISCH, Gerald
; MUELLER, Guenter
; TITLE OF INVENTION: USE OF LEPTIN ANTAGONISTS FOR TREATING
; INSULIN RESISTANCE IN TYPE II DIABETES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,805
; FILING DATE: 14-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/05035
; FILING DATE: 15-SEP-1997
; APPLICATION NUMBER: DE 196 38 487.7
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 03e083/0200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
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Best Local Similarity 100.0%; Pred. No. 9.3e-88;
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QY 121 WASGLETLDSLGGLVLEASGYSTEVVALSRLOGLSQDMLWQDLSPGC 167
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RESULT 15
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; Sequence 4, Application US/08438431A
; Patent No. 6429290
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAFFEI,
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,431A
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6429290ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide
; ORIGINAL SOURCE: Human
US-08-438-431A-4

Query Match 100.0%; Score 870; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLGFLWLPYLFVQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

Qy 61 DFIFGLHPILTSLKMDQTLAVYQOILTSMPSRNVIOISNDLENLRDLHLVAFSKSCHLP 120
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Qy 121 WASGLETLDSLGGLVLEASGYSTEVVALSRQGSIQDMLWQLDLSFGC 167
Db 121 WASGLETLDSLGGLVLEASGYSTEVVALSRQGSIQDMLWQLDLSFGC 167

Search completed: March 12, 2005, 05:05:39
Job time : 33.5463 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2005, 05:03:46 ; Search time 93.9042 Seconds
(without alignments)
586.599 Million cell updates/sec

Title: US-10-049-182-4

Perfect score: 870
Sequence: 1 MHWGTLGFLWLPYFVQ.....SRLOGSLQMLWQLDLPQC 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	870	100.0	167	9 US-09-789-306-3	Sequence 3, Appli
4	870	100.0	167	9 US-09-804-409A-11	Sequence 11, Appli
5	870	100.0	167	10 US-09-316-393-4	Sequence 4, Appli
6	870	100.0	167	15 US-10-440-464-67	Sequence 67, Appli
7	870	100.0	167	15 US-10-458-334-17	Sequence 17, Appli
8	870	100.0	167	17 US-10-698-510-17	Sequence 17, Appli
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38	733	84.3	146	16 US-10-658-834A-676	Sequence 682, Appli
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40	731	84.0	146	9 US-09-850-433-4	Sequence 674, Appli
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ALIGNMENTS

RESULT 1

US-09-736-084-4
; Sequence 4, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/736,084

FILING DATE: 13-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/438,431

FILING DATE: May 10, 1995

APPLICATION NUMBER: 08/347,563

FILING DATE: No. US20020107211A1, September 30, 1994

APPLICATION NUMBER: 08/292,345

FILING DATE: August 17, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-736-084-4
Query Match 100.0%; Score 870; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MHWGTLGGLWLPYLFYVQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLKSKMDQTLAVYQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 120
Db 61 DFIPGLHPILTLKSKMDQTLAVYQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 120
QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGLQSLQDMLWQLDLSFGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGLQSLQDMLWQLDLSFGC 167
;
; RESULT 2
; US-09-928-522-7
; Sequence 7, Application US/09928522
; Patent No. US20020110857A1
; GENERAL INFORMATION:
; APPLICANT: Spurlock, Michael E.
; TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID
; SEQUENCES CODING THEREFOR AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.
; STREET: Suite 2100 111 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/928,522
; FILING DATE: 13-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,908
; FILING DATE: 31-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plotecher, Gary R.
; REGISTRATION NUMBER: 27,830
; REFERENCE/DOCKET NUMBER: PM-8808
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 414-223-2100
; TELEFAX: 414-223-5000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; Query Match 100.0%; Score 870; DB 9; Length 167;
; Best Local Similarity 100.0%; Pred. No. 2.7e-84;
; Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 MHWGTLGGLWLPYLFYVQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 60
; Db 1 MHWGTLGGLWLPYLFYVQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 60
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-928-522-7
Query Match 100.0%; Score 870; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHWGTLGGLWLPYLFYVQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGGLWLPYLFYVQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLKSKMDQTLAVYQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 120
Db 61 DFIPGLHPILTLKSKMDQTLAVYQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 120
QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGLQSLQDMLWQLDLSFGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGLQSLQDMLWQLDLSFGC 167
;
; RESULT 3
; US-09-789-306-3
; Sequence 3, Application US/09789306
; Patent No. US20020142456A1
; GENERAL INFORMATION:
; APPLICANT: Heritday, Nataasha
; TITLE OF INVENTION: Canine OB Protein Compositions and
; METHODS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,306
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,408
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Eggert, Joan D.
; REFERENCE/DOCKET NUMBER: A-387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Leader Sequence
; LOCATION: -21 to -1
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-789-306-3
Query Match 100.0%; Score 870; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 MHWGTLGGLWLPYLFYVQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 60
; Db 1 MHWGTLGGLWLPYLFYVQVPIQKVQDDTKLTIKTIVTRINDISHTQSVSSKQKVTGL 60
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QY 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
DB 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSGPC 167

RESULT 4
US-09-804-409A-11
; Sequence 11, Application US/09804409A
; Patent No. US20020155100A1
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, TIMOTHY J.
; APPLICANT: CHEUNG, ANTHONY T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
; TITLE OF INVENTION: EXPRESSION IN GUT
; FILE REFERENCE: 029996/027 8721
; CURRENT APPLICATION NUMBER: US/09/804,409A
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-409A-11

Query Match 100.0%; Score 870; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
DB 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSGPC 167

RESULT 5
US-09-316-393-4
; Sequence 4, Application US/09316393
; Publication No. US20030040039A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/316,393
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
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; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human Ob protein
; ORIGINAL SOURCE: Human
US-09-316-393-4

Query Match 100.0%; Score 870; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
DB 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSGPC 167

RESULT 6
US-10-440-464-67
; Sequence 67, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 67
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-67

Query Match 100.0%; Score 870; DB 15; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
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Db 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLKTIIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLLHLVAFSKSCHLP 120
Db 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLLHLVAFSKSCHLP 120
QY 121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167
Db 121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167

RESULT 7
US-10-458-334-17
; Sequence 17, Application US/10458334
; Publication No. US20040043932A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Patricia G
; APPLICANT: Lee, Daniel W.
; TITLE OF INVENTION: Leptin-Related Peptides
; FILE REFERENCE: AMC-1 Leptin Peptides (19705-001)
; CURRENT APPLICATION NUMBER: US/10/458,334
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US/09/377,081
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/097,457
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-458-334-17

Query Match 100.0%; Score 870; DB 15; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLKTIIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLLHLVAFSKSCHLP 120
Db 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLLHLVAFSKSCHLP 120
QY 121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167
Db 121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167

RESULT 8
US-10-698-510-17
; Sequence 17, Application US/10698510
; Publication No. US20050049193A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Patricia
; APPLICANT: Lee, Daniel
; APPLICANT: Leinung, Matthew
; TITLE OF INVENTION: Leptin Related Peptides
; FILE REFERENCE: 19705-001CIP
; CURRENT APPLICATION NUMBER: US/10/698,510
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/422,723
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 09/377,081
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 167

Query Match 100.0%; Score 870; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 8.9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-510-17

Query Match 100.0%; Score 870; DB 17; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLCGFLWLPYLFYVQAVPIQKVQDDTKTLKTIIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLLHLVAFSKSCHLP 120
Db 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLLHLVAFSKSCHLP 120
QY 121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167
Db 121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167

RESULT 9
US-09-859-361-2
; Sequence 2, Application US/09859361
; Patent No. US20020058311A1
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael
; APPLICANT: Chapman, Conrad
; APPLICANT: Clinkenberg, Helen
; APPLICANT: Robinson, Jeffrey
; TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin
; Domain and Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,361
; FILING DATE: 17-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,783
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P31202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-859-361-2

Query Match 100.0%; Score 870; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 8.9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTLKMDQTLAVYQVQILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSCHLP 120
Db 61 DFIPGLHPILTLKMDQTLAVYQVQILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSCHLP 120
Qy 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
Db 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
RESULT 10
US-09-859-361-5
; Sequence 5, Application US/09859361
; Patent No. US20020058311A1
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael
; Chapman, Conrad
; Clinkenbeard, Helen
; Robinson, Jeffrey
; TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin
; Domain and Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,361
; FILING DATE: 17-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/991,783
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P31202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-859-361-5
Query Match 100.0%; Score 870; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 8.9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTLKMDQTLAVYQVQILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSCHLP 120
Db 61 DFIPGLHPILTLKMDQTLAVYQVQILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSCHLP 120

Qy 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
Db 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
RESULT 11
US-08-779-457-47
; Sequence 47, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-779-457-47
Query Match 100.0%; Score 870; DB 8; Length 397;
Best Local Similarity 100.0%; Pred. No. 8.9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTLKMDQTLAVYQVQILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSCHLP 120
Db 61 DFIPGLHPILTLKMDQTLAVYQVQILTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSCHLP 120
Qy 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
Db 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
RESULT 12
US-10-921-710-47

; Sequence 47, Application US/10921710
; Publication No. US20050019325A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Matthews, William
; TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIBODIES THAT
; TITLE OF INVENTION: DECREASE BODY WEIGHT, FAT-DEPOT WEIGHT OR FOOD INTAKE IN AN
; TITLE OF INVENTION: OBESE ANIMAL
; FILE REFERENCE: GENENT.53CP2C1
; CURRENT APPLICATION NUMBER: US/10/921,710
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 08/779457
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 60/064855
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/585005
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/667197
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-710-47

Query Match 100.0%; Score 870; DB 17; Length 397;
Best Local Similarity 100.0%; Pred. No. 8.9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWTGTCGFLWLPYLVVQAVPIQKVQDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWTGTCGFLWLPYLVVQAVPIQKVQDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60

Qy 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLLHLVLAFSKSHLP 120
Db 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLLHLVLAFSKSHLP 120

Qy 121 WASGLETLDLSGGVLEASGYSTEVVALSRQGSLODMLWQLDLSGPC 167
Db 121 WASGLETLDLSGGVLEASGYSTEVVALSRQGSLODMLWQLDLSGPC 167

RESULT 13
US-09-859-361-7
; Sequence 7, Application US/09859361
; Patent No. US20020058311A1
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael
; Chapman, Conrad
; Clinckenbeard, Helen
; Robinson, Jeffrey
; TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin
; Domain and Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,361
; FILING DATE: 17-May-2001

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,783
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P31202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-859-361-7

Query Match 100.0%; Score 870; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWTGTCGFLWLPYLVVQAVPIQKVQDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWTGTCGFLWLPYLVVQAVPIQKVQDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60

Qy 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLLHLVLAFSKSHLP 120
Db 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLLHLVLAFSKSHLP 120

Qy 121 WASGLETLDLSGGVLEASGYSTEVVALSRQGSLODMLWQLDLSGPC 167
Db 121 WASGLETLDLSGGVLEASGYSTEVVALSRQGSLODMLWQLDLSGPC 167

RESULT 14
US-09-859-361-9
; Sequence 9, Application US/09859361
; Patent No. US20020058311A1
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael
; Chapman, Conrad
; Clinckenbeard, Helen
; Robinson, Jeffrey
; TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin
; Domain and Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,361
; FILING DATE: 17-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,783
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P31202

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-859-361-9

Query Match 100.0%; Score 870; DB 9; Length 401;

Best Local Similarity 100.0%; Pred. No. 9.1e-84;

Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLGFLWLPYLVVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

Db 1 MHWGTLGFLWLPYLVVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

Qy 61 DFIPGLHPILTLSKMDQTLAVYQOILTSMPSRNVQISNDLENLRLDLLHVLAFSKSCHLP 120

Db 61 DFIPGLHPILTLSKMDQTLAVYQOILTSMPSRNVQISNDLENLRLDLLHVLAFSKSCHLP 120

Qy 121 WASGLETDSLGGLVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167

Db 121 WASGLETDSLGGLVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167

RESULT 15

US-09-736-084-6

Sequence 6, Application US/09736084

Patent No. US20020107211A1

GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY

TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/736,084

FILING DATE: 13-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/438,431

FILING DATE: May 10, 1995

APPLICATION NUMBER: 08/347,563

FILING DATE: No. US20020107211A1, November 30, 1994

APPLICATION NUMBER: 08/292,345

FILING DATE: August 17, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: Human ob polypeptide lacking Gln at position

ORIGINAL SOURCE:

ORGANISM: Human

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-736-084-6

Query Match 98.2%; Score 854.5; DB 9; Length 166;

Best Local Similarity 99.4%; Pred. No. 1.2e-82;

Matches 166; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MHWGTLGFLWLPYLVVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

Db 1 MHWGTLGFLWLPYLVVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 59

Qy 61 DFIPGLHPILTLSKMDQTLAVYQOILTSMPSRNVQISNDLENLRLDLLHVLAFSKSCHLP 120

Db 60 DFIPGLHPILTLSKMDQTLAVYQOILTSMPSRNVQISNDLENLRLDLLHVLAFSKSCHLP 119

Qy 121 WASGLETDSLGGLVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167

Db 120 WASGLETDSLGGLVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 166

Search completed: March 12, 2005, 05:21:03

Job time : 94.9042 secs

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